

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:28:48 ; Search time 17 Seconds
(without alignments)
548.268 Million cell updates/sec

Title: US-10-050-552A-2
Perfect score: 903
Sequence: 1 MAAQLQSVSFLMGTLATSC.....EIKAGELDLLFMSLRNACI 179

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	897	99.3	179	1 IL22_HUMAN	Q9gzx6 homo sapien
2	718	79.5	179	1 IL22_MOUSE	Q9jyy9 mus musculu
3	714	79.1	179	1 I22B_MOUSE	Q9jyy8 mus musculu
4	106.5	11.8	179	1 IL10_CEREL	P51746 cervus elap
5	105.5	11.7	178	1 IL10_MACFA	P79338 macaca fasc
6	103	11.4	170	1 BCRF_BBV	P03180 epstein-bar
7	101.5	11.2	178	1 IL10_CERTO	P46651 cercocebus
8	101.5	11.2	178	1 IL10_MACMU	P51496 macaca mula
9	99.5	11.0	183	1 MOB5_RAT	Q9ji24 rattus norv
10	96.5	10.7	178	1 IL10_HUMAN	P22301 homo sapien
11	96.5	10.7	178	1 IL10_MARMO	Q9jhh7 marmota mon
12	95.5	10.6	178	1 IL10_FELCA	P55029 felis silve
13	95.5	10.6	178	1 IL10_MACNE	P51497 macaca neme
14	95	10.5	178	1 IL10_BOVIN	P43480 bos taurus
15	93	10.3	174	1 IL10_TRIVU	Q97798 trichosurus
16	90.5	10.0	178	1 IL10_MOUSE	P18893 mus musculu
17	89.5	9.9	178	1 IL10_HORSE	Q28374 equus cabal
18	89.5	9.9	181	1 IL10_CANFA	P48411 canis famil
19	87	9.6	175	1 IL10_PIG	Q29055 sus scrofa
20	86	9.5	206	1 IL24_HUMAN	Q13007 homo sapien
21	85	9.4	177	1 IL10_SHEEP	Q29408 ovis aries
22	84.5	9.4	164	1 IL10_ORCOR	O46673 orcinus orc
23	84.5	9.4	178	1 IL10_RAT	P29456 rattus norv
24	84	9.3	171	1 IL26_HUMAN	Q9nph9 homo sapien
25	82	9.1	2184	1 RRPL_CDVO	P24658 canine dist
26	81.5	9.0	178	1 IL10_CAVPO	Q921y5 cavia porce
27	80	8.9	569	1 PYRD_PLAFA	Q08210 plasmodium
28	79.5	8.8	178	1 IL10_MERUN	P47965 meriones un
29	79.5	8.8	294	1 Y237_MYCGE	P47479 mycoplasma
30	79.5	8.8	1391	1 N157_YEAST	P40064 saccharomyc
31	78.5	8.7	879	1 AMD2_HUMAN	Q01433 homo sapien
32	78	8.6	176	1 IL20_HUMAN	Q9nyy1 homo sapien
33	77	8.5	214	1 PITX_RHIME	Q30498 rhizobium m

RESULT 1
IL22_HUMAN
ID IL22_HUMAN STANDARD; PRT; 179 AA.
AC Q9GZX6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-22 precursor (IL-22) (IL-10-related T-cell-derived
DE inducible factor) (IL-TIF) (UNQ3099/PRO10096).
GN IL22 OR ILTIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20420346; PubMed=10954742;
RA Dumoutier L., Van Roost E., Colau D., Renauld J.-C.;
RT "Human interleukin-10-related T cell-derived inducible factor:
RT molecular cloning and functional characterization as an hepatocyte-
RT stimulating factor."
RL Proc. Natl. Acad. Sci. U.S.A. 97:10144-10149(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21069354; PubMed=11197690;
RA Dumoutier L., Van Roost E., Colau D., Ameye G., Michaux L.,
RA Renauld J.-C.;
RT "IL-TIF/IL-22: genomic organization and mapping of the human and mouse
RT genes."
RL Genes Immun. 1:488-494(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20469498; PubMed=10875937;
RA Xie M.-H., Aggarwal S., Ho W.-H., Foster J., Zhang Z., Stinson J.,
RA Wood W.I., Goddard A.D., Gurney A.L.;
RT "Interleukin (IL)-22, a novel human cytokine that signals through the
RT interferon receptor-related proteins CRF2-4 and IL-22R."
RL J. Biol. Chem. 275:31335-31339(2000).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT GLY-158.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale

ALIGNMENTS

34	76	8.4	179	1	IL10_HSVE2	Q89451 equine herp
35	76	8.4	245	1	UBIE_BACTN	Q8a005 bacteroides
36	76	8.4	518	1	TT8_ARATH	Q9ft81 arabidopsis
37	75.5	8.4	691	1	EFG2_SYNY3	P74228 synechocyst
38	75	8.3	369	1	KAPR_STRPU	Q26619 strongyloce
39	75	8.3	917	1	DML3_ARATH	Q49498 arabidopsis
40	74.5	8.3	430	1	PSMR_METJA	Q58576 methanococc
41	74.5	8.3	4451	1	GRSB_BACBR	P14688 b gramicidi
42	74	8.2	439	1	SYH_CLOTE	Q892x7 clostridium
43	74	8.2	553	1	MCRA_METVA	P07961 methanococc
44	73.5	8.1	361	1	YG59_METJA	Q59053 methanococc
45	73.5	8.1	928	1	NIBA_HUMAN	Q9bzq8 homo sapien

RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
CC -!- FUNCTION: Cytokine that contributes to the inflammatory response
CC in vivo.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-10 family.
CC -----
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CC -----
DR EMBL; AJ277247; CAC06085.1; -.
DR EMBL; AJ277248; CAC19409.1; -.
DR EMBL; AF279437; AAG22064.1; -.
DR EMBL; AF387519; AAG62468.1; -.
DR EMBL; AY358890; AAQ89249.1; -.
DR Genew; HGNC:14900; IL22.
DR MIM; 605330; -.
DR GO; GO:0005576; C:extracellular; IC.
DR GO; GO:0045518; F:interleukin-22 receptor binding; NAS.
DR GO; GO:0006953; P:acute-phase response; NAS.
DR GO; GO:0007267; P:cell-cell signaling; IC.
DR GO; GO:0006954; P:inflammatory response; NAS.
DR InterPro; IPR000098; Interleukin_10.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
KW Cytokine; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 179 INTERLEUKIN-22.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 158 158 S -> G.
FT /FTID=VAR 013078.
SQ SEQUENCE 179 AA; 20011 MW; 3C35E64D60CF8767 CRC64;

Query Match 99.3%; Score 897; DB 1; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.7e-78;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSFLMGTLATSCLLALLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLA 60
Db 1 MAALQKSVSFLMGTLATSCLLALLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLA 60

QY 61 KEASLADNNTDVRLLIGELKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
Db 61 KEASLADNNTDVRLLIGELKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120

QY 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAIKIGELDLFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAIKIGELDLFMSLRNACI 179

RESULT 2
IL22_MOUSE
ID IL22_MOUSE STANDARD; PRT; 179 AA.
AC Q9JUJ9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-22 precursor (IL-22) (IL-10-related T-cell-derived
DE inducible factor) (IL-TIF) (IL-TIF alpha) (Interleukin-22a) (IL-22a).
GN IL22 OR IL22A OR ILTIFA OR ILTIF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=AKR;
RX MEDLINE=20126044; PubMed=10657629;
RA Dumoutier L., Louahed J., Renaud J.-C.;
RT "Cloning and characterization of IL-10-related T cell-derived
RT inducible factor (IL-TIF), a novel cytokine structurally related to
RT IL-10 and inducible by IL-9";
RL J. Immunol. 164:1814-1819(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=21069354; PubMed=11197690;
RA Dumoutier L., Van Roost E., Colau D., Ameye G., Michaux L.,
RA Renaud J.-C.;
RT "IL-TIF/IL-22: genomic organization and mapping of the human and mouse
RT genes.";
RL Genes Immun. 1:488-494(2000).
CC -!- FUNCTION: Cytokine that contributes to the inflammatory response
CC in vivo.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-10 family.
CC -----
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CC -----
DR EMBL; AJ249491; CAB75546.1; -.
DR EMBL; AJ294727; CAC19435.1; -.
DR MGD; MGI:1355307; IL22.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006800; P:oxygen and reactive oxygen species metabolism; IDA.
DR GO; GO:0042516; P:regulation of tyrosine phosphorylation of S. . .; IDA.
DR InterPro; IPR000098; Interleukin_10.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 179 INTERLEUKIN-22.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 179 AA; 20106 MW; ACB0F5574AA79274 CRC64;

Query Match 79.5%; Score 718; DB 1; Length 179;
Best Local Similarity 76.5%; Pred. No. 4.6e-61;
Matches 137; Conservative 22; Mismatches 20; Indels 0; Gaps 0;

QY 1 MAALQKSVSFLMGTLATSCLLALLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLA 60
Db 1 MAALQKSVSFLMGTLATSCLLALLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLA 60

QY 61 KEASLADNNTDVRLLIGELKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
Db 61 KEASLADNNTDVRLLIGELKLFHGVSAKQCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120

QY 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAIKIGELDLFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAIKIGELDLFMSLRNACI 179

RESULT 3
IL22_MOUSE
ID IL22_MOUSE STANDARD; PRT; 179 AA.
AC Q9JUJ8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-22 precursor (IL-22b) (IL-10-related T-cell-derived
DE inducible factor beta) (IL-TIFb) (IL-TIF beta).
GN IL22B OR ILTIFB.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=20126044; PubMed=10657629;
RA Dumoutier L., Louahed J., Renauld J.-C.;
RT "Cloning and characterization of IL-10-related T cell-derived
RT inducible factor (IL-TIF), a novel cytokine structurally related to
RT IL-10 and inducible by IL-9";
RL J. Immunol. 164:1814-1819(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=21069354; PubMed=11197690;
RA Dumoutier L., Van Roost E., Colau D., Ameye G., Michaux L.,
RA Renauld J.-C.;
RT "IL-TIF/IL-22: genomic organization and mapping of the human and mouse
RT genes.";
RL Genes Immun. 1:488-494(2000).
CC -!- FUNCTION: Cytokine that contributes to the inflammatory response
CC in vivo.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-10 family.
CC -----
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CC -----
DR EMBL; AJ249492; CAB75547.1; -.
DR EMBL; AJ294728; CAC19436.1; -.
DR MGD; MGI:2151139; Il10f.
DR InterPro; IPR000098; Interleukin_10.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 179 INTERLEUKIN-22B.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 179 AA; 20162 MW; 4425498580DA5F60 CRC64;
Query Match 79.1%; Score 714; DB 1; Length 179;
Best Local Similarity 76.0%; Pred. No. 1.1e-60;
Matches 136; Conservative 23; Mismatches 20; Indels 0; Gaps 0;
QY 1 MAALQKSVSFLMGTLATSCLLALLVQGGAAPISSHCRLDKSNFQOPYITNRTFMLA 60
DB 1 MAVLQKSMFSLSMGTAAASCLLLIALWAQANALPINTCKLEVSNFQOPYIVNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
DB 61 KEASLADNNTDVRLLIGEKLFGVSAKQCYLMKQVLFNFTLEDILLPQSDRFQPYMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDLLHIQNVQKLKDTVKKIGESGEIKALGELDLFLMSLRNACI 179
DB 121 FLTKLSNQLSSCHISGDDQNTQKNVRLKETVKKLGESGEIKALGELDLFLMSLRNACV 179
RESULT 4
ID IL10_CEREL STANDARD; PRT; 179 AA.
AC P51746;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory

DE factor) (CSIP).
GN IL10.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96063015; PubMed=7579578;
RA Lockhart E., Slobbe L., Droogmans L., Griffin F., Buchan G.;
RT "The cloning and sequencing of cervine interleukin 10.";
RL DNA Seq. 5:265-268(1995).
CC -!- FUNCTION: Inhibits the synthesis of a number of cytokines,
CC including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by
CC activated macrophages and by helper T cells (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-10 family.
CC -----
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CC -----
DR EMBL; U11767; AAA85434.1; -.
DR HSSP; P22301; 1INR.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0005141; F:interleukin-10 receptor binding; NAS.
DR GO; GO:0006916; P:anti-apoptosis; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTERLEUKIN10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 179 INTERLEUKIN-10.
FT DISULFID 31 127 BY SIMILARITY.
FT DISULFID 81 133 BY SIMILARITY.
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 179 AA; 20467 MW; A1C0035D484B6050 CRC64;
Query Match 11.8%; Score 106.5; DB 1; Length 179;
Best Local Similarity 22.8%; Pred. No. 0.0051;
Matches 41; Conservative 32; Mismatches 74; Indels 33; Gaps 6;
QY 20 CLLLLA-LLVQGGAAPISSHCRLDKSNFQOPYITNRTFMLAKEASLA-----DN 68
DB 10 CLVFLAGVAASRDASAPSDSSC-----THFSNLSPLMLRELRTAFSRVKNFFQMKD 60
QY 69 NTDVRLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVPFIAR---- 124
DB 61 QLDLSMLLTQSLDDDFKGYLGQALSEMIQFYLEEVN-POAENHGPEIKHVNLSGELKLT 119
QY 125 ISNRLSTCHIEGDDLLHIQNVQKLKDTVKKIGESGEIKALGELDLFL-----MSLRN 176
DB 120 LRRLRRCHRFPLPCENKSKAVEQVSKVFSKLQERGVIKAMSEFDIFINYIETTTMKKN 179
RESULT 5
ID IL10_MACFA
AC P79338;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory

RT *Cloning, sequencing of human interleukin-10 cDNA and construction of
RT its eukaryotic expression vector."
RL Harbin Yike Daxue Xue Bao 35:4-6(2001).
[4]
RP SEQUENCE FROM M.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE OF 26-34 AND 170-178.
RX MEDLINE=98070801; PubMed=9405662;
RA Gesser B., Jeffers H., Jinquan T., Vestergaard C., Kirstein N.,
RA Sindert-Pedersen S., Jensen S.L., Thstrup-Pedersen K., Larsen C.G.;
RT "Identification of functional domains on human interleukin 10.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:14620-14625(1997).
[6]
RP DISULFIDE BONDS.
RX MEDLINE=93372085; PubMed=8364028;
RA Windsor W.T., Syto R., Tsarobopoulos A., Zhang R., Durkin J.,
RA Baldwin S., Paliwal S., Mui P.W., Pramanik B., Trotta P.P.;
RT "Disulfide bond assignments and secondary structure analysis of human
RL and murine interleukin 10.";
RN Biochemistry 32:8807-8815(1993).
[7]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=96032603; PubMed=7547951;
RA Walter M.R., Nagabhushan T.L.;
RT "Crystal structure of interleukin 10 reveals an interferon gamma-like
RL fold.";
RN Biochemistry 34:12118-12125(1995).
[8]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX MEDLINE=96173008; PubMed=8590020;
RA Zdanov A., Schalk-Hihi C., Gustchina A., Tsang M., Wheatherbee J.,
RA Wlodawer A.;
RT "Crystal structure of interleukin-10 reveals the functional dimer
RL with an unexpected topological similarity to interferon gamma.";
RN Structure 3:591-601(1995).
[9]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RX MEDLINE=97052966; PubMed=8897595;
RA Zdanov A., Schalk-Hihi C., Wlodawer A.;
RT "Crystal structure of human interleukin-10 at 1.6-A resolution and a
RL model of a complex with its soluble receptor.";
RN Protein Sci. 5:1955-1962(1996).
[10]
RP VARIANT CD ARG-15.
RX MEDLINE=22709749; PubMed=12825869;
RA van der Linde K., Boor P.P., Sandkuijl L.A., Meijssen M.A.,
RA Savelkoul H.F., Wilson J.H., de Rooij F.W.;
RT "A Gly15Arg mutation in the interleukin-10 gene reduces secretion of
RL interleukin-10 in Crohn disease.";
RN Scand. J. Gastroenterol. 38:611-617(2003).
CC -!- FUNCTION: Inhibits the synthesis of a number of cytokines,
CC including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by
CC activated macrophages and by helper T cells.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by a variety of cell lines, including
CC T cells, macrophages, mast cells and other cell types.
CC -!- DISEASE: Defects in IL10 are a cause of susceptibility to
CC Crohn's disease (CD) [MIM:266600], a form of remitting
CC inflammatory bowel disease (IBD). CD may involve any part of the
CC gastrointestinal tract, but most frequently the terminal ileum and
CC colon. Bowel inflammation is transmural and discontinuous. Crohn's
CC disease is commonly classified as autoimmune disease.
CC -!- SIMILARITY: Belongs to the IL-10 family.

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CC
CC
CC
DR EMBL; M57627; AAA63207.1; --
DR EMBL; U16720; AAA80104.1; --
DR EMBL; AY029171; AAK38162.1; --
DR EMBL; AF418271; AAL06594.1; --
DR FIR; A38580; A38580.
DR PDB; 1ILK; 10-JUL-95.
DR PDB; 2ILK; 14-OCT-96.
DR PDB; 1INR; 14-OCT-96.
DR PDB; 1J7V; 19-SEP-01.
DR PDB; 1LK3; 17-JUL-02.
DR Genew; HGNC:5962; IL10.
DR MIM; 124092; --
DR MIM; 266600; --
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0008189; F:apoptosis inhibitor activity; NAS.
DR GO; GO:0005125; F:cytokine activity; TAS.
DR GO; GO:0005141; F:interleukin-10 receptor binding; NAS.
DR GO; GO:0006916; P:anti-apoptosis; NAS.
DR GO; GO:0030183; P:B-cell differentiation; NAS.
DR GO; GO:0042100; P:B-cell proliferation; NAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0007253; P:cytoplasmic sequestering of NF-kappaB; NAS.
DR GO; GO:0030097; P:hemopoiesis; TAS.
DR GO; GO:0006954; P:inflammatory response; NAS.
DR GO; GO:0045355; P:negative regulation of interferon-alpha bio. . . ; NAS.
DR GO; GO:0045077; P:negative regulation of interferon-gamma bio. . . ; ISS.
DR GO; GO:0045347; P:negative regulation of MHC class II biosynt. . . ; TAS.
DR GO; GO:0045019; P:negative regulation of nitric oxide biosynt. . . ; ISS.
DR GO; GO:0042130; P:negative regulation of T-cell proliferation; NAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR GO; GO:0045191; P:regulation of isotype switching; NAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR GO; GO:0042092; P:T-helper 2 type immune response; TAS.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTERLEUKIN10.
DR PRODOM; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
KW Cytokine; Glycoprotein; Signal; Disease mutation; 3D-structure.
FT SIGNAL 1 18
FT CHAIN 19 178 INTERLEUKIN-10.
FT DISULFID 30 126
FT DISULFID 80 132
FT CARBOHYD 134 134
FT VARIANT 15 15
FT TURN 33 36
FT HELIX 37 49
FT TURN 50 51
FT HELIX 52 58
FT HELIX 68 75
FT TURN 77 78
FT HELIX 79 93
FT TURN 94 94
FT HELIX 95 99
FT TURN 100 101
FT TURN 103 105
FT HELIX 106 125
FT TURN 127 128
FT HELIX 131 133
FT HELIX 137 148
FT TURN 149 150
FT HELIX 151 159
FT TURN 160 160
FT HELIX 161 176
SQ SEQUENCE 178 AA; 20517 MW; 6825E9FA4337CDE4 CRC64;

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or send an email to license@isb-sib.ch).

N-LINKED (GLCNAC. . .) (POTENTIAL).
G -> R (in CD; decreases secretion
thereby reducing the anti-inflammatory
effect).
/FTId=VAR_015883.


```
DR GO: 0007253; P:cytoplasmic sequestering of NF-kappaB; ISS.
DR GO: 0030097; P:hemoipoiesis; ISS.
DR GO: 0006954; P:inflammatory response; ISS.
DR GO: 0045077; P:negative regulation of interferon-gamma bio. . .; ISS.
DR GO: 0045347; P:negative regulation of MHC class II biosynt. . .; ISS.
DR GO: 0045019; P:negative regulation of nitric oxide biosynt. . .; ISS.
DR GO: 0042130; P:negative regulation of T-cell proliferation; ISS.
DR GO: 0045191; P:regulation of isotype switching; ISS.
DR GO: 0042092; P:T-helper 2 type immune response; ISS.
DR GO: 0007260; P:tyrosine phosphorylation of STAT protein; ISS.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTRLEUKIN10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 178 INTERLEUKIN-10.
FT DISULFID 30 126 BY SIMILARITY.
FT DISULFID 80 132 BY SIMILARITY.
FT CARBOHYD 29 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 178 AA; 20529 MW; 836C9635D9C185AA CRC64;

Query Match 10.6%; Score 95.5; DB 1; Length 178;
Best Local Similarity 29.4%; Pred. No. 0.056;
Matches 25; Conservative 20; Mismatches 35; Indels 5; Gaps 2;

QY 89 CYLMQVLFLEEVLPQSDRFQPMQEVVPPFIAR-----ISNRLSTCHIEGDDLHIQRN 144
Db 80 QALSEMIQFYLEEVM-PQAEENEDPDIKQHVNSLGEKLTLLRLRRCHRFPCENKSKV 138
* QY 145 VQKLKDTVKKIGESGEIKAIGELDL 169
Db 139 VEQVKSTFSLQEKGVYKAMGEFDI 163

* RESULT 13
IL10_MACNE STANDARD; PRT; 178 AA.
AC P51497;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory factor) (CSIF).
DE IL10.
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PT 10000;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates."
RL J. Immunol. 155:3946-3954 (1995).
CC -!- FUNCTION: Inhibits the synthesis of a number of cytokines, including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by activated macrophages and by helper T cells (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-10 family.
CC -----
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CC -----
DR EMBL; L26031; AAA99976.1; -.
DR HSSP; P22301; 1INR.
DR GO: 0005576; C:extracellular; ISS.
DR GO: 0008189; F:apoptosis inhibitor activity; ISS.
DR GO: 0005141; F:interleukin-10 receptor binding; ISS.
DR GO: 0006916; P:anti-apoptosis; ISS.
DR GO: 0030183; P:B-cell differentiation; ISS.
DR GO: 0042100; P:B-cell proliferation; ISS.
DR GO: 0007253; P:cytoplasmic sequestering of NF-kappaB; ISS.
DR GO: 0030097; P:hemoipoiesis; ISS.
DR GO: 0006954; P:inflammatory response; ISS.
DR GO: 0045077; P:negative regulation of interferon-gamma bio. . .; ISS.
DR GO: 0045347; P:negative regulation of MHC class II biosynt. . .; ISS.
DR GO: 0045019; P:negative regulation of nitric oxide biosynt. . .; ISS.
DR GO: 0042130; P:negative regulation of T-cell proliferation; ISS.
DR GO: 0045191; P:regulation of isotype switching; ISS.
DR GO: 0042092; P:T-helper 2 type immune response; ISS.
DR GO: 0007260; P:tyrosine phosphorylation of STAT protein; ISS.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTRLEUKIN10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 178 INTERLEUKIN-10.
FT DISULFID 30 126 BY SIMILARITY.
FT DISULFID 80 132 BY SIMILARITY.
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 178 AA; 20560 MW; 35CC0D9D49E70718 CRC64;

Query Match 10.6%; Score 95.5; DB 1; Length 178;
Best Local Similarity 23.2%; Pred. No. 0.056;
Matches 39; Conservative 30; Mismatches 76; Indels 23; Gaps 5;

QY 18 TSCLLLLALLVQGAAP-----ISSHRLDKSN-----FQPYITNRTFMLEASL 65
Db 3 SSALLCCLVLLTGVRASPGQGTQSENSCTRFPGNLPMLRLDLDAFSRVKTFQMKD--- 59
QY 66 ADNNTDVRLLIGELKLFHGVSMSERCYLMQVLFLEEVLPQSDRFQPMQEVVPPFIAR- 124
Db 60 ---QLDNILLKESLLEDFKGYLGCOALSEMIQFYLEEVM-PQAEHNDPDIKEHVNSLGEN 115
QY 125 ---ISNRLSTCHIEGDDLHIQNVQKLKDTVKKIGESGEIKAIGELDL 169
Db 116 LKTLRLRLRRCHRFPCENKSKAVEQVMNAPSKLQEKGVYKAMSEFDI 163

RESULT 14
IL10_BOVIN STANDARD; PRT; 178 AA.
AC P43480;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory factor) (CSIF).
DE IL10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Charolais; TISSUE=Blood;
RX MEDLINE=94156210; PubMed=8112615;
RA Hash S.M., Brown W.C., Rice-Ficht A.C.;
RT "Characterization of a cDNA encoding bovine interleukin 10: kinetics
```

```

RT of expression in bovine lymphocytes." ;
RL Gene 139:257-261(1994).
CC -!- FUNCTION: Inhibits the synthesis of a number of cytokines,
CC including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by
CC activated macrophages and by helper T cells (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-10 family.
CC -----
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CC -----
DR EMBL; U03799; AAA19011.1; -.
DR HSSP; P22301; 1INR.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0008189; F:apoptosis inhibitor activity; ISS.
DR GO; GO:0005141; F:interleukin-10 receptor binding; ISS.
DR GO; GO:0006916; P:anti-apoptosis; ISS.
DR GO; GO:0030183; P:B-cell differentiation; ISS.
DR GO; GO:0042100; P:B-cell proliferation; ISS.
DR GO; GO:0007253; P:cytoplasmic sequestering of NF-kappaB; ISS.
DR GO; GO:0030097; P:hemopoiesis; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0042095; P:interferon-gamma biosynthesis; IMP.
DR GO; GO:0045077; P:negative regulation of interferon-gamma bio. . ; NAS.
DR GO; GO:0045347; P:negative regulation of MHC class II biosynt. . ; ISS.
DR GO; GO:0045019; P:negative regulation of nitric oxide biosynt. . ; NAS.
DR GO; GO:0042130; P:negative regulation of T-cell proliferation; ISS.
DR GO; GO:0045191; P:regulation of isotype switching; ISS.
DR GO; GO:0042092; P:T-helper 2 type immune response; ISS.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTRLEUKIN10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
DR Cytokine; Glycoprotein; Signal.
DR SIGNAL 1 18 POTENTIAL.
DR CHAIN 19 178 INTERLEUKIN-10.
DR DISULFID 30 126 BY SIMILARITY.
DR DISULFID 80 132 BY SIMILARITY.
DR CARBOHYD 134 134 N-LINKED (GLCNAC...) (POTENTIAL).
DR SEQUENCE 178 AA; 20411 MW; BAD6D176BD9D056 CRC54;

Query Match 10.5%; Score 95; DB 1; Length 178;
Best Local Similarity 24.1%; Pred. No. 0.062;
Matches 40; Conservative 32; Mismatches 74; Indels 20; Gaps 6;

QY 19 SCILLALLVQGGAAPISSHCRLDKSNFQPYITNRTFMLAK-EASLADNNTDVRLLIGE 77
Db 3 SSALLCCLVFLAGVAASRDASTLSDSSCTHLP--TSLPHMLRELRAAFGEAKTFQFM--K 58

QY 78 KLFHGVSMSESR-----CYLMKQVNLFTLEEVLPQSDRFQPYMQEVVPPFIAR--- 124
Db 59 DQLHSLLLTQSLDDDFKGYLGQALSEMIQFYLEEVM-POAENHGPDIKEHVNSLGEK 117

QY 125 -ISNRLSTCHIEGDDLLHIQNVQKLDKTVKKIGESGEIKAGELDL 169
Db 118 TLRLRLRCHRFPCENKSKAVEKVRVSELSQERGVYKAMSEFDI 163

RESULT 15
IL10 TRIVU
ID IL10 TRIVU STANDARD; PRT; 174 AA.
AC O97798;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

```

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DE Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory
DE factor) (CSIF).
GN IL10.
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99449065; PubMed=10520755;
RA Wedlock D.N., Aldwell F.E., Buddle B.M.;
RT "Nucleotide sequence of a marsupial interleukin-10 cDNA from the
RT Australian brushtail possum (Trichosurus vulpecula).";
RL DNA Seq. 9:239-244(1998).
CC -!- FUNCTION: Inhibits the synthesis of a number of cytokines,
CC including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by
CC activated macrophages and by helper T cells (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-10 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF026277; AAD01799.1; -.
DR HSSP; P22301; 1INR.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTRLEUKIN10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
DR Cytokine; Glycoprotein; Signal.
DR SIGNAL 1 16 POTENTIAL.
DR CHAIN 17 174 INTERLEUKIN-10.
DR DISULFID 26 122 BY SIMILARITY.
DR DISULFID 76 128 BY SIMILARITY.
DR CARBOHYD 17 17 N-LINKED (GLCNAC...) (POTENTIAL).
DR SEQUENCE 174 AA; 20262 MW; DA838DBF74DF9C06 CRC64;

Query Match 10.3%; Score 93; DB 1; Length 174;
Best Local Similarity 22.2%; Pred. No. 0.094;
Matches 35; Conservative 37; Mismatches 74; Indels 12; Gaps 6;

QY 21 LLLALL--VQGGAAPISSHCRLDKSNFQPYITNR-TFMLAKEASLADNNTDVRLLIGE 77
Db 5 MLLFCLLCVTSSNLSSALEDNCKTFSTTLPNMLRELRAAFSSVKTFFQTRDKLETKLIDK 64

QY 78 KLFHGVSMSESRCYLMKQVNLFTLEEVLPQSDRFQPYMQEVVPPFIAR----ISNRLSTCH 133
Db 65 SLLEELKSYLGQALSEMIKFYLEEVM-PRAEENELDVKEDVGSIGELKALRLRLKRC 123

QY 134 --IEGDDLHIQNVQKLDKTVKKIGESGEIKAGELDL 169
Db 124 RFLPCED--NSRVVQVRNTYKELQEQGVYKAMGDFDI 159

Search completed: June 30, 2004, 19:34:35
Job time : 19 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:32:59 ; Search time 41 Seconds
(without alignments)
1377.506 Million cell updates/sec

Title: US-10-050-552A-2
Perfect score: 903
Sequence: 1 MAALQKSVSFLMGTMTSC.....EIKAGELDLLFMSLRNACI 179

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	116.5	12.9	175	13 Q7SX60	Q7sx60 tetraodon n
2	111.5	12.3	183	13 Q802T4	Q802t4 fugu rubrip
3	106.5	11.8	178	11 Q80WE8	Q80we8 peromyscus
4	106	11.7	181	13 Q7SX82	Q7sx82 tetraodon n
5	104	11.5	177	12 Q8UJ36	Q8uzj6 cercopithec
6	99.5	11.0	171	12 Q9Q5L1	Q9q5l1 herpesvirus
7	98.5	10.9	178	6 Q8MKG9	Q8mkg9 saimiri sci
8	97.5	10.8	220	11 Q925J3	Q925j3 mus musculu
9	97	10.7	184	13 Q7ZSY8	Q7zsy8 tetraodon n
10	96	10.6	180	13 Q7T3I1	Q7t3i1 cyprinus ca
11	95.5	10.6	178	6 Q9TSJ7	Q9tsj7 felis silve
12	95.5	10.6	181	11 Q925S4	Q925s4 mus musculu
13	95.5	10.6	183	11 Q9WVP8	Q9wvp8 rattus norv
14	94	10.4	178	6 Q9TSJ4	Q9tsj4 oryctolagus
15	92.5	10.2	131	11 Q9ERG7	Q9er97 peromyscus
16	90.5	10.0	103	11 Q88646	Q88646 marmota mon

17	90.5	10.0	178	6 Q9TVD3	Q9tvd3 oryctolagus
18	90.5	10.0	178	6 Q865X4	Q865x4 lama glama
19	88	9.7	170	12 Q91MZ9	Q91mz9 lumpy skin
20	87.5	9.7	130	11 O70327	O70327 mesocricetu
21	86.5	9.6	754	16 Q99ZC3	Q99zc3 streptococc
22	86.5	9.6	754	16 Q8P0K7	Q8p0k7 streptococc
23	86.5	9.6	754	16 Q8K752	Q8k752 streptococc
24	85.5	9.5	189	12 Q80G59	Q80g59 bovine papu
25	85.5	9.5	601	16 Q8ZIG5	Q8zig5 yersinia pe
26	85	9.4	141	10 Q40849	Q40849 picea glauc
27	83.5	9.2	324	2 Q83Z76	Q83z76 citrobacter
28	83.5	9.2	437	9 Q9AZM2	Q9azm2 bacterioph
29	83.5	9.2	437	16 Q9CI94	Q9ci94 lactococcus
30	82.5	9.1	961	11 Q80W87	Q80w87 rattus norv
31	82	9.1	463	11 Q8BLA4	Q8bla4 mus musculu
32	82	9.1	934	11 Q8C0U7	Q8cou7 mus musculu
33	82	9.1	2184	12 Q9DXZ1	Q9dxz1 canine dist
34	82	9.1	2184	12 P87575	P87575 canine dist
35	82	9.1	2752	5 Q9BJY0	Q9bjy0 plasmodium
36	81.5	9.0	122	6 Q95LE3	Q95le3 canis famil
37	81.5	9.0	758	16 Q8DT31	Q8dt31 streptococc
38	80.5	8.9	275	5 Q8IIV0	Q8iiv0 plasmodium
39	80.5	8.9	932	5 O15924	O15924 dictyosteli
40	79.5	8.8	160	11 Q923T1	Q923t1 sigmodon hi
41	79.5	8.8	186	12 O11386	O11386 orf virus (
42	79.5	8.8	186	12 O11387	O11387 orf virus (
43	79.5	8.8	186	12 Q80G31	Q80g31 orf virus.
44	79.5	8.8	188	16 Q81CW3	Q81cw3 bacillus ce
45	79.5	8.8	319	16 Q92H29	Q92h29 rickettsia

ALIGNMENTS

RESULT 1				
Q7SX60				
ID	Q7SX60	PRELIMINARY;	PRT;	175 AA.
AC	Q7SX60;			
DT	01-OCT-2003 (TrEMBLrel. 25, Created)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Interleukin-20.			
GN	IL20.			
OS	Tetraodon nigroviridis (Green puffer).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;			
OC	Tetraodontoidea; Tetraodontidae; Tetraodon.			
OX	NCBI_TaxID=99883;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Lutfalla G., Roest Crollius H., Stange-Thomann N., Jaillon O.,			
RA	Mogense K., Monneron D.;			
RT	"Independent expansion of a lineage-specific gene family in			
RT	vertebrates: The class II cytokine receptors and their ligands in			
RT	mammals and fish."			
RL	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY294557; AAP57414.1; -.			
DR	EMBL; AY294558; AAP57416.1; -.			
SQ	SEQUENCE 175 AA; 19838 MW; DE6FA67E0038ED34 CRC64;			
Query Match 12.9%; Score 116.5; DB 13; Length 175;				
Best Local Similarity 24.9%; Pred. NO. 0.0013;				
Matches 43; Conservative 30; Mismatches 85; Indels 15; Gaps 7;				
QY	13	MGTLATSCLLLLALLV---QGGAAPISCHRLDKSNFQQPYITNRTFMFLAKEASLADNN	69	
Db	1	MKTLPISCLLFLALCCLTEBAQSTLLVDSCTI-SADLQEMHQHNSNRL--NAITDEE	57	
QY	70	TDVRLIGEKLFGHGVSMSERCYLMKQVLNFTLEVL-----FPQSDRFQPYMQEVVPFIA	123	
Db	58	IGVKLLSKRLMEDVQDQRCCLRLVLQFYIDRVFPSPYLSLSSHPQNSSSSSSLANTFIIV	117	

QY 124 RISNRLSFCHIEGDDHLHIQNVQKLDKTVKIGES-GEIKAIGELDLFMSLR 175
 Db 118 R-KQMIQKCHLCEQ-ETQKKVDSLLDAFNKLEASKAVLKAVGELDTVLQWLQ 168

RESULT 2

ID Q802T4 PRELIMINARY; PRT; 183 AA.
 AC Q802T4;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Interleukin 10 homologue precursor.
 GN IL10.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zou J., Clark M.S., Secombes C.J.;
 RT *Characterisation, expression and promoter analysis of an interleukin
 RT 10 homologue in the puffer fish, Fugu rubripes*;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ539537; CAD62446.1; -.
 DR GO:0005576; C:extracellular; IEA.
 DR GO:0005125; F:Cytokine activity; IEA.
 DR GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000098; Interleukin_10.
 DR Pfam; PF00726; IL10; 1.
 DR PRINTS; PR01294; INTRLEUKIN10.
 DR ProDom; PD003687; Interleukin_10; 1.
 DR SMART; SM00188; IL10; 1.
 KW Signal.
 FT SIGNAL
 SQ SEQUENCE 1 21 POTENTIAL.
 SEQUENCE 183 AA; 21076 MW; 5DCF5667E8F6B404 CRC64;

Query Match 12.3%; Score 111.5; DB 13; Length 183;
 Best Local Similarity 22.6%; Pred. No. 0.0044;
 Matches 40; Conservative 33; Mismatches 73; Indels 31; Gaps 5;

QY 19 SCLLLALLVQGGAAPISSHC-----RLDKSNFQOPYITNRTFMLEKASLAD 67
 Db 8 SVLLLLCCACTWCAALCNRCSCFVEGFPARLKMRENYSQ-----IRDYEEAN 57
 QY 68 NNTDVLRLGEKLFHGVSMSERCYLMKQVLFNFTLEVL-----FPQSDRFQPYMQEVP 120
 Db 58 DDLDIVLDDQSIQVDTFTKTPFACHLMDGILRFYDSVLPALATVTAETRNKPKHVESIQ 117
 QY 121 FIARISNRLSTC-HIEGDDHLHIQNVQKLDKTVKIGESGEIKAIGELDLFMSLRN 176
 Db 118 IFDQLKIEVTNCKHYFACKNRFDINV--LNSTYTKMEDKGLYKAMGELDLFNYIEN 172

RESULT 3

Q80WE8 PRELIMINARY; PRT; 178 AA.
 ID Q80WE8
 AC Q80WE8;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Interleukin-10.
 GN IL10.
 OS Peromyscus maniculatus (Deer mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 OC Peromyscus.
 OX NCBI_TaxID=10042;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Carruthers T., Herbst M.M., Schountz T.;

RT "Genomic organization of the deer mouse interleukin-10 gene."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY251293; AAP13853.1; -.
 DR GO:0005576; C:extracellular; IEA.
 DR GO:0005125; F:Cytokine activity; IEA.
 DR GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000098; Interleukin_10.
 DR Pfam; PF00726; IL10; 1.
 DR PRINTS; PR01294; INTRLEUKIN10.
 DR ProDom; PD003687; Interleukin_10; 1.
 DR SMART; SM00188; IL10; 1.
 DR PROSITE; PS00520; INTERLEUKIN_10; 1.
 SQ SEQUENCE 178 AA; 20504 MW; 270044CIA7E8C1FC CRC64;

Query Match 11.8%; Score 106.5; DB 11; Length 178;
 Best Local Similarity 24.1%; Pred. No. 0.014;
 Matches 45; Conservative 34; Mismatches 69; Indels 39; Gaps 8;

QY 14 GTLATSCLLLALLVQGGAA-----PISSHCRLD--KSNFQOPYITNRTFM 58
 Db 3 GSAPLCCLLLLA---EVGASRGHNTQEGNCTHPPVSQTYTLRELFADFQV---XTFF 55
 QY 59 LAKEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLEPQSDRFQPYMQEV 118
 Db 56 QKXD-----QLDSILLTDSLMKDPKGYLGQALSEMIFQVLFVEM-PQAEHGHGPEIKEH 108
 QY 119 VPFIAR-----ISNRLSTCHIEGDDHLHIQNVQKLDKTVKIGESGEIKAIGELDLL--- 170
 Db 109 LNFLGEKLTLLRRRLQCHRFPCENKSKAVEQVKSDFENKQNGVYKAMSEDFINCI 168
 QY 171 --FMSLR 175
 Db 169 EAYMTIR 175

RESULT 4

Q7SX82 PRELIMINARY; PRT; 181 AA.
 ID Q7SX82
 AC Q7SX82;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Interleukin-24.
 GN IL24.
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lutfalla G., Roest Crollius H., Stange-Thomann N., Jaillon O.,
 RA Mogense K., Monneron D.;
 RT *Independent expansion of a lineage-specific gene family in
 RT vertebrates: The class II cytokine receptors and their ligands in
 RT mammals and fish*;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY294559; AAP57417.1; -.
 DR EMBL; AY294560; AAP57418.1; -.
 SQ SEQUENCE 181 AA; 20610 MW; 0EC5ABD39A6EBFD3 CRC64;

Query Match 11.7%; Score 106; DB 13; Length 181;
 Best Local Similarity 26.8%; Pred. No. 0.016;
 Matches 45; Conservative 30; Mismatches 73; Indels 20; Gaps 7;

QY 21 LLLALLVQGGAAAPISSHCRDKSNFQOPYITNRTFM---LAKEASLADNNTDVRLLIG 76
 Db 16 LLAVSLIGWSELAPV---HLPHKALSPPLDDQTHKAVEEVANQAQLEQDDPSVRLMP 71
 QY 77 EKLHF---GVSMSERCYLMKQVLFNFTLEEVLEPQSDRFQPYMQEVPFIARISNRLST-- 131
 Db 72 ----HPPAGPDNLEICCLHANILDFYLLNVLSSHSTDNQ-HTRRLRSDLRSISHDLEAHG 126

QY 132 CHIEGDLHIQNVQKLDKTVKKGESGEIKAGELDLFMSLRNACI 179
 Db 127 CNI--TRYHDHQHAKVFRQRFEGHGRHTKALGEVDILFYLYQDYCV 172

RESULT 5

Q8UZJ6 PRELIMINARY; PRT; 177 AA.
 AC Q8UZJ6;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE BCRF1.
 CS Cercopithecine herpesvirus 15.
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC Gammaherpesvirinae; Lymphocryptovirus.
 OX NCBI_TaxID=104228;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LCL8664;
 RX MEDLINE=97048062; PubMed=8892903;
 RA Franken M., Devergne O., Rosenzweig M., Annis B., Kieff E., Wang F.;
 RT "Comparative analysis identifies conserved tumor necrosis factor
 RT receptor-associated factor 3 binding sites in the human and simian
 RT Epstein-Barr virus oncogene LMPL.";
 RL J. Virol. 70:7819-7826(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LCL8664;
 RX MEDLINE=99412410; PubMed=10482645;
 RA Rivallier P., Quirk C., Wang F.;
 RT "Strong selective pressure for evolution of an Epstein-Barr virus
 RT LMP2B homologue in the rhesus lymphocryptovirus.";
 RL J. Virol. 73:8867-8872(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LCL8664;
 RX MEDLINE=20304984; PubMed=10846073;
 RA Jiang H., Cho Y.-G., Wang F.;
 RT "Structural, functional, and genetic comparisons of Epstein-Barr virus
 RT nuclear antigen 3A, 3B, and 3C homologues encoded by the rhesus
 RT lymphocryptovirus.";
 RL J. Virol. 74:5921-5932(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LCL8664;
 RX MEDLINE=20440633; PubMed=10970361;
 RA Rao P., Jiang H., Wang F.;
 RT "Cloning of the rhesus lymphocryptovirus viral capsid antigen and
 RT Epstein-Barr virus-encoded small RNA homologues and use in diagnosis
 RT of acute and persistent infections.";
 RL J. Clin. Microbiol. 38:3219-3225(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LCL8664;
 RX MEDLINE=21602573; PubMed=11739708;
 RA Rivallier P., Jiang H., Cho Y.-G., Quirk C., Wang F.;
 RT "Complete Nucleotide Sequence of the Rhesus Lymphocryptovirus: Genetic
 RT Validation for an Epstein-Barr Virus Animal Model.";
 RL J. Virol. 76:421-426(2002).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LCL8664;
 RA Moghaddam A., Koch J., Annis B., Wang F.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LCL8664;
 RA Moghaddam A., Annis B., Wang F.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.

RC STRAIN=LCL8664;
 RA Rivallier P., Quirk C., Wang F.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LCL8664;
 RA Jiang H., Wang F.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LCL8664;
 RA Rao P.V., Jiang H., Wang F.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LCL8664;
 RA Rivallier P., Jiang H., Cho Y.-G., Quirk C., Wang F.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY037858; AAK95412.1; -.
 DR HSSP; P22301; 2ILK.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000098; Interleukin_10.
 DR Pfam; PF00726; IL10; 1.
 DR PRINTS; PR01294; INTRLEUKIN10.
 DR ProDom; PD003687; Interleukin_10; 1.
 DR SMART; SM00188; IL10; 1.
 DR PROSITE; PS00520; INTERLEUKIN_10; 1.
 SQ SEQUENCE 177 AA; 20545 MW; 5F94050532E63A36 CRC64;

Query Match 11.5%; Score 104; DB 12; Length 177;
 Best Local Similarity 24.6%; Pred. No. 0.024;
 Matches 41; Conservative 30; Mismatches 80; Indels 16; Gaps 5;

QY 12 LMGTLATSCLLLLALLVQ---GGAAAPISSHCHRLDK--SNFQOPYITNRTFMLAKEASLA 66
 Db 3 LRSGLTLQCLVILQCLVLMYLAAPACKGVSNCGNLFHMLRLDLDAFSRVKTFQMKD---- 58
 QY 67 DNNTDVRLLIGKLFHGVSMSEHCYLMKQVLFNFTLEEVLPQSDRFQPMQEVVPPFIAR-- 124
 Db 59 --QLDNILLKESLLEDFKGLGCGQALSEMIQFYLEEVV-PQAEHQDPHAKHVNLSIGENL 115
 QY 125 --ISNRLSTCHIEGDDLHIQNVQKLDKTVKKGESGEIKAGELDL 169
 Db 116 KTLRLRLRRCHRFPLPCENKSKAVEQVKNFAFKLQKGVYKAMSEFDI 162

RESULT 6

Q9Q5L1 PRELIMINARY; PRT; 171 AA.
 AC Q9Q5L1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE VIL10.
 OS Herpesvirus papio.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Lymphocryptovirus.
 OX NCBI_TaxID=10394;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Baboon lymphocryptovirus BA65;
 RA Zong J.-C., Ryan J., Ling P.D., Loeb D.D., Pagano J.S., Hayward S.D.,
 RA Hayward G.S.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF200364; AAF23949.1; -.
 DR HSSP; P22301; IINR.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000098; Interleukin_10.
 DR Pfam; PF00726; IL10; 1.


```
Matches 42; Conservative 28; Mismatches 68; Indels 37; Gaps 8;
QY 20 CLLLALL--VOGGAAP--SSHCRLDKSNFQPPYITNRTFMLEKEASLADNNTDRLI 75
Db 10 CLSLLILLNQVPLEGQEFRRSGCQV--TGVLPDLWEAFWTVKNTVQTDDITSIRLL 67
QY 76 GEKLFHGVSMSERCYLMKQVLFLEWLFPSQDRFQPMQEVVPPFIARISNRLSTCHIE 135
Db 68 KPQVLRNVSGAESCYLAHSLKLYLNTV-----FKNYHSKIAKF--KVLRSFST--LA 116
QY 136 GDDLHIQNVQKLD--TVKKIGESGE-----IKAIGELDLL 170
Db 117 NNFIVMSQLQPSKDNMLPISBSAHQRLFRFAFKQLDTEWLVKAFGEVDIL 171

RESULT 13
Q9WVP8
ID Q9WVP8 PRELIMINARY; PRT; 183 AA.
AC Q9WVP8;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE C49a.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=99308986; PubMed=10381256;
RA Soc C., Shaw W.M., Freymiller E., Longaker M.T., Bertolami C.N.,
RA Chiu R., Tieu A., Ting K.;
RT "Cutaneous rat wounds express c49a, a novel gene with homology to the
RT human melanoma differentiation associated gene, mda-7.";
RL J. Cell. Biochem. 74:1-10(1999).
DR EMBL; AF004774; AAB69171.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000098; Interleukin_10.
DR ProDom; PD003687; Interleukin_10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
SQ SEQUENCE 183 AA; 21052 MW; FF69A96AFC473E4F CRC64;

Query Match 10.6%; Score 95.5; DB 11; Length 183;
Best Local Similarity 26.9%; Pred. No. 0.18;
Matches 35; Conservative 19; Mismatches 45; Indels 31; Gaps 5;
QY 67 DNNTDVRLLIGEKLFGVSMSERCYLMKQVLFLEWLFPSQDRFQPMQEVVPPFIARIS 126
Db 61 DELTSARLLKPKQVQLQNVSDAESCYLAHSLKLYLNTV-----FKNYHSKIVKF--KVL 111
QY 127 NRLSTCHIEGDDLHIQNVQKLD-----TVKKIG-ESGEIKAGE 166
Db 112 KSFST--LANNFLVMSKIQPSKDNAMLPISDSARRRFLFHRTFKQLDIEVALAKAFGE 163
QY 167 LLLFMSLRN 176
Db 170 VDLIAWMQN 179

RESULT 14
Q9TSJ4
ID Q9TSJ4 PRELIMINARY; PRT; 178 AA.
AC Q9TSJ4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Interleukin-10.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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OX NCBI_TaxID=9936;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RX MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RT European rabbit (Oryctolagus cuniculus).";
RL Cytokine 12:555-565(2000).
DR EMBL; AF068058; AAC23839.1; -.
DR HSSP; P22301; 1INR.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTRLEUKIN10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
SQ SEQUENCE 178 AA; 20146 MW; A5E0B2A8F04D5170 CRC64;

Query Match 10.4%; Score 94; DB 6; Length 178;
Best Local Similarity 22.0%; Pred. No. 0.24;
Matches 37; Conservative 30; Mismatches 77; Indels 24; Gaps 4;
QY 19 SCLLLALLVQGGAAAPISSHCRCLKSNFQPP-----YITNRTFMLEKEASL 65
Db 3 SSALLCCLVFLGGTGASRGQDTPAENSCHFFPGGLPHMLRELRAAFGRVKTFFQSKD--- 59
QY 66 ADNNTDVRLLIGEKLFGVSMSERCYLMKQVLFLEWLFPSQDRFQPMQEVVPPFIAR- 124
Db 60 ---QLNSMLLTESLLEDLAGYLGCQALSEMIQFYLYKQVM-PQAEHNSPAIREHVNLSGEN 115
QY 125 ---ISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAGELDL 169
Db 116 LKTLRLRLRQCHRFPCENKSKAVEQVKSFAFKLQEEGVYKAMSEFDI 163

RESULT 15
Q9ERG7
ID Q9ERG7 PRELIMINARY; PRT; 131 AA.
AC Q9ERG7;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Interleukin-10 (Fragment).
GN IL10.
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Herbst M.M., Schountz T.;
RT "Cloning of the deer mouse interferon gamma, interleukin-10 and tumor
RT necrosis factor genes.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF307012; AAG30263.1; -.
DR HSSP; P22301; 1INR.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTRLEUKIN10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
FT NON_TER 1
FT NON_TER 131
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:27:38 ; Search time 23 Seconds
(without alignments)
401.785 Million cell updates/sec

Title: US-10-050-552A-2
Perfect score: 903
Sequence: 1 MAALQKSVSFLMGTATSC.....EIKAI GELDLLFMSLRNACI 179

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCITUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	897	99.3	179	4	US-09-870-574-2
2	875	96.9	179	4	US-09-419-568F-28
3	875	96.9	179	4	US-09-354-243B-28
4	718	79.5	179	3	US-09-178-973B-15
5	718	79.5	179	4	US-09-419-568F-27
6	718	79.5	179	4	US-09-354-243B-27
7	714	79.1	179	3	US-09-178-973B-16
8	103	11.4	170	1	US-08-270-805C-2
9	103	11.4	170	2	US-08-410-654B-2
10	103	11.4	170	2	US-08-474-851-2
11	103	11.4	170	2	US-08-481-560-2
12	103	11.4	170	2	US-08-934-959-4
13	103	11.4	170	3	US-08-170-113-2
14	103	11.4	170	3	US-08-765-094C-26
15	103	11.4	170	3	US-09-082-797-26
16	103	11.4	170	3	US-08-643-810A-2
17	103	11.4	170	4	US-09-552-613-2
18	103	11.4	170	4	US-09-512-256-26
19	98.5	10.9	154	4	US-09-452-624A-3
20	97.5	10.8	220	3	US-08-884-077-2
21	96.5	10.7	178	1	US-08-270-805C-1
22	96.5	10.7	178	2	US-08-410-654B-1
23	96.5	10.7	178	2	US-08-474-851-1
24	96.5	10.7	178	2	US-08-481-560-1
25	96.5	10.7	178	2	US-08-934-959-6
26	96.5	10.7	178	3	US-08-170-113-1
27	96.5	10.7	178	3	US-08-765-094C-25

28	96.5	10.7	178	3	US-09-082-797-25	Sequence 25, Appli
29	96.5	10.7	178	3	US-08-643-810A-1	Sequence 1, Appli
30	96.5	10.7	178	4	US-09-552-613-1	Sequence 1, Appli
31	96.5	10.7	178	4	US-09-512-256-25	Sequence 25, Appli
32	96.5	10.7	178	4	US-09-462-941-16	Sequence 16, Appli
33	92.5	10.2	147	1	US-08-270-805C-4	Sequence 4, Appli
34	92.5	10.2	147	2	US-08-410-654B-4	Sequence 4, Appli
35	92.5	10.2	147	2	US-08-474-851-4	Sequence 4, Appli
36	92.5	10.2	147	2	US-08-481-560-4	Sequence 4, Appli
37	92.5	10.2	147	3	US-08-170-113-4	Sequence 4, Appli
38	92.5	10.2	147	3	US-08-643-810A-4	Sequence 4, Appli
39	92.5	10.2	147	4	US-09-552-613-4	Sequence 4, Appli
40	92.5	10.2	147	5	PCT-US93-07646-2	Sequence 2, Appli
41	92.5	10.2	166	4	US-09-452-624A-4	Sequence 4, Appli
42	91.5	10.1	160	1	US-08-270-805C-3	Sequence 3, Appli
43	91.5	10.1	160	2	US-08-410-654B-3	Sequence 3, Appli
44	91.5	10.1	160	2	US-08-474-851-3	Sequence 3, Appli
45	91.5	10.1	160	2	US-08-481-560-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-870-574-2
; Sequence 2, Application US/09870574
; Patent No. 6551799
; GENERAL INFORMATION:
; APPLICANT: Gurney, Austin L.
; APPLICANT: Aggarwal, Sudeepta
; APPLICANT: Xie, Ming-Hong
; APPLICANT: Maruoka, Ellen M.
; APPLICANT: Foster, Jessica S.
; APPLICANT: Goddard, Audrey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: INTERLEUKIN-22 POLYPEPTIDES, NUCLEIC ACIDS ENCODING
; FILE REFERENCE: P2806-1{US}
; CURRENT APPLICATION NUMBER: US/09/870,574
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 60/169,495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 2
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-870-574-2

Query Match 99.3%; Score 897; DB 4; Length 179;
Best Local Similarity 98.3%; Pred. No. 2.2e-100;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAALQKSVSFLMGTATSCILLALLVQGGAAAPISSHCRDKSNFQPYITNRTFMLA 60	
Db	1	MAALQKSVSFLMGTATSCILLALLVQGGAAAPISSHCRDKSNFQPYITNRTFMLA 60	
QY	61	KEASLADNNTDVRLLIGEKLFHGVSMSERCYLKQVLTLEVLFPQSDRFQPYMQEVVP 120	
Db	61	KEASLADNNTDVRLLIGEKLFHGVSMSERCYLKQVLTLEVLFPQSDRFQPYMQEVVP 120	
QY	121	FIARISNRLSTCHIEGDDLHIQORNQKLDKTVKKIGESGEIKAIGELDLLFMSLRNACI 179	
Db	121	FIARISNRLSTCHIEGDDLHIQORNQKLDKTVKKIGESGEIKAIGELDLLFMSLRNACI 179	

RESULT 2
US-09-419-568F-28
; Sequence 28, Application US/09419568F

Patent No. 6331613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
TITLE OF INVENTION: (Tifs) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 28
LENGTH: 179
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
US-09-419-568F-28

Query Match 96.9%; Score 875; DB 4; Length 179;
Best Local Similarity 96.1%; Pred. No. 9.9e-98;
Matches 172; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISCHCRLDKSNFQQPYITNRTFMLA 60
Db 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISCHCRLDKSNFQQPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLSEVLPQSDRFRPYMQEVVP 120
Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLSEVLPQSDRFRPYMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAGELDLLEFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAGELDLLEFMSLRNACI 179

RESULT 3
US-09-354-243B-28
Sequence 28, Application US/09354243B
Patent No. 6359117
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
TITLE OF INVENTION: (Tifs)
TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 28
LENGTH: 179
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
US-09-354-243B-28

Query Match 96.9%; Score 875; DB 4; Length 179;
Best Local Similarity 96.1%; Pred. No. 9.9e-98;
Matches 172; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISCHCRLDKSNFQQPYITNRTFMLA 60
Db 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISCHCRLDKSNFQQPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLSEVLPQSDRFRPYMQEVVP 120

Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLSEVLPQSDRFRPYMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAGELDLLEFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAGELDLLEFMSLRNACI 179
RESULT 4
US-09-178-973B-15
Sequence 15, Application US/09178973B
Patent No. 6274710
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
TITLE OF INVENTION: (Tifs)
TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543
CURRENT APPLICATION NUMBER: US/09/178,973B
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 15
LENGTH: 179
TYPE: PRT
ORGANISM: Mus musculus
US-09-178-973B-15

Query Match 79.5%; Score 718; DB 3; Length 179;
Best Local Similarity 76.5%; Pred. No. 9.5e-79;
Matches 137; Conservative 22; Mismatches 20; Indels 0; Gaps 0;
QY 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISCHCRLDKSNFQQPYITNRTFMLA 60
Db 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISCHCRLDKSNFQQPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLSEVLPQSDRFRPYMQEVVP 120
Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLSEVLPQSDRFRPYMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAGELDLLEFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAGELDLLEFMSLRNACI 179

RESULT 5
US-09-419-568F-27
Sequence 27, Application US/09419568F
Patent No. 6331613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
TITLE OF INVENTION: (Tifs) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 27
LENGTH: 179
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
US-09-419-568F-27

Query Match 79.5%; Score 718; DB 4; Length 179;
Best Local Similarity 76.5%; Pred. No. 9.5e-79;
Matches 137; Conservative 22; Mismatches 20; Indels 0; Gaps 0;

QY 1 MAALQKSVSFLMGTATSCILLALLVOGGAAPISCHRLDKSNFQOQPYITNRTFMLA 60
Db 1 MAVLQKSMSPSLMGTATSCILLALLVOGGAAPISCHRLDKSNFQOQPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGELKLFHGVSMSEKCYLMKQVLFNFTLEEVLPQSDRFQPYMGEVVP 120
Db 61 KEASLADNNTDVRLLIGELKLFHGVSAKQCYLMKQVLFNFTLEEVLPQSDRFQPYMGEVVP 120
QY 121 FIARISNRLSTCHIEGDLHIQNVQKLDKTVKKGESGEIKAIKELDLFMSLRNACI 179
Db 121 FLTKLSNQLSSCHISGDDQNIQKNVRLKETVKKLGESGEIKAIKELDLFMSLRNACV 179

RESULT 6
US-09-354-243B-27
; Sequence 27, Application US/39354243B
; Patent No. 6359117
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Louhed, Jamila
; APPLICANT: Renault, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
; TITLE OF INVENTION: (TIFS)
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543.1
; CURRENT APPLICATION NUMBER: US/09/354,243B
; PRIOR FILING DATE: 1999-07-16
; PRIOR FILING DATE: US09/178,973
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 27
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
US-09-354-243B-27

Query Match 79.5%; Score 718; DB 4; Length 179;
Best Local Similarity 76.5%; Pred. No. 9.5e-79; Indels 0; Gaps 0;
Matches 137; Conservative 22; Mismatches 20;
QY 1 MAALQKSVSFLMGTATSCILLALLVOGGAAPISCHRLDKSNFQOQPYITNRTFMLA 60
Db 1 MAVLQKSMSPSLMGTATSCILLALLVOGGAAPISCHRLDKSNFQOQPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGELKLFHGVSMSEKCYLMKQVLFNFTLEEVLPQSDRFQPYMGEVVP 120
Db 61 KEASLADNNTDVRLLIGELKLFHGVSAKQCYLMKQVLFNFTLEEVLPQSDRFQPYMGEVVP 120
QY 121 FIARISNRLSTCHIEGDLHIQNVQKLDKTVKKGESGEIKAIKELDLFMSLRNACI 179
Db 121 FLTKLSNQLSSCHISGDDQNIQKNVRLKETVKKLGESGEIKAIKELDLFMSLRNACV 179

RESULT 7
US-09-178-973B-16
; Sequence 16, Application US/09178973B
; Patent No. 6274710
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Louhed, Jamila
; APPLICANT: Renault, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
; TITLE OF INVENTION: (TIFS)
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543
; CURRENT APPLICATION NUMBER: US/09/178,973B
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 179
; TYPE: PRT

; ORGANISM: Mus musculus
US-09-178-973B-16
Query Match 79.1%; Score 714; DB 3; Length 179;
Best Local Similarity 76.0%; Pred. No. 2.9e-78;
Matches 136; Conservative 23; Mismatches 20; Indels 0; Gaps 0;
QY 1 MAALQKSVSFLMGTATSCILLALLVOGGAAPISCHRLDKSNFQOQPYITNRTFMLA 60
Db 1 MAVLQKSMSPSLMGTATSCILLALLVOGGAAPISCHRLDKSNFQOQPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGELKLFHGVSMSEKCYLMKQVLFNFTLEEVLPQSDRFQPYMGEVVP 120
Db 61 KEASLADNNTDVRLLIGELKLFHGVSAKQCYLMKQVLFNFTLEEVLPQSDRFQPYMGEVVP 120
QY 121 FIARISNRLSTCHIEGDLHIQNVQKLDKTVKKGESGEIKAIKELDLFMSLRNACI 179
Db 121 FLTKLSNQLSSCHISGDDQNIQKNVRLKETVKKLGESGEIKAIKELDLFMSLRNACV 179

RESULT 8
US-08-270-805C-2
; Sequence 2, Application US/08270805C
; Patent No. 5776451
; GENERAL INFORMATION:
; APPLICANT: Di-Hwei Hsu
; APPLICANT: Kevin K. Moore
; APPLICANT: Hergen Spits
; TITLE OF INVENTION: Use of Interleukin10 in Adoptive Immunotherapy
; TITLE OF INVENTION: of Cancer
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7.5.3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/270,805C
; FILING DATE: 05-July-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/995,564
; FILING DATE: 23-Dec-1992
; APPLICATION NUMBER: US 07/830,493
; FILING DATE: 04-Feb-1992
; APPLICATION NUMBER: US 07/641,342
; FILING DATE: 16-Jan-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: DX0142Q2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-298-2987
; TELEFAX: 908-298-5388
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-270-805C-2

Query Match 11.4%; Score 103; DB 1; Length 170;
Best Local Similarity 24.8%; Pred. No. 0.0002;
Matches 40; Conservative 27; Mismatches 68; Indels 26; Gaps 6;


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STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,797
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/765,094
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0800/94
FILING DATE: 05-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: GRONHOJ-LARSEN=1
TELEPHONE: (202)628-5197
TELEFAX: (202)737-3528
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-082-797-26

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	Query Match	11.4%; Score 103; DB 3; Length 170;
	Best Local Similarity	24.8%; Pred. No. 0.0002;
	Matches 40; Conservative 27; Mismatches 68; Indels 26; Gaps 6;	
QY	20 CLALLALLVQGGAAPISSHCRLLDKSNFQQ-----PYTNRTFMLAKEASLADNNTDV 72 :: : : : :: :	
Dd	11 CLVLLYLAPECGG---TDQC----DNFPQMLRLDLDAFSRVKTFQTQKD-----EVDN 56 :: : : : :: :	
QY	73 RLIGEKLFHGVSMSERCYLMKQVLNFTLEEVLPQSDFRQPVMQVEVPFIAR----ISNR 128 :: : : : :: :	
Dd	57 LLLKESLLEDFFXGILGCQALSEMIQFYLEEVM-POAENQDPPEAKDHVNSLGENTKLTLRLR 115 :: : : : :: :	
QY	129 LSTCHIEGDDLHIQRNVQKLKDTVKKIGESGEIKAI GELDL 169 : : :: : : : :	
Dd	116 LRRCHRFLPCNKSKAVEQIKNFAFNKLQEKGIYKAMSEFDI 156 : : :: : : : :	

Search completed: June 30, 2004, 19:34:04
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:26:48 ; Search time 20 Seconds
{without alignments}
860.914 Million cell updates/sec

Title: US-10-050-552A-2
Perfect score: 903
Sequence: 1 MAALQKSVSFLMGTLATSC.....EIKAI GELDEL FMSLRNACI 179

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	11.4	170	1 QQBE2	BCRF1 protein - hu
2	96.5	10.7	178	2 A38580	interleukin-10 pre
3	90.5	10.0	178	2 A34853	interleukin-10 pre
4	87	9.6	175	2 I46591	interleukin 10 - p
5	86.5	9.6	178	2 JN3475	interleukin-10 pre
6	85.5	9.5	601	2 AG0066	probable AMP-bindi
7	85	9.4	141	2 TQ2251	embryonic abundan
8	83.5	9.2	437	2 H86683	prophage pil prote
9	82	9.1	2161	1 A45389	genome polypeptid
10	79.5	8.8	294	1 B64226	hypothetical prote
11	79.5	8.8	319	2 G97817	magnesium and cba
12	79.5	8.8	683	2 E71845	polyribonucleotide
13	79.5	8.8	683	2 E64671	polynucleotide pho
14	79.5	8.8	1391	2 S50608	hypothetical prote
15	78.5	8.7	605	2 S59996	AMP deaminase (EC
16	78.5	8.7	760	2 A44313	AMP deaminase (EC
17	78	8.6	232	2 T28369	probable uracil-DN
18	77.5	8.6	326	2 D84719	hypothetical prote
19	77	8.5	357	2 D82292	phospho-2-dehydro-
20	76.5	8.5	660	2 S66708	probable membrane
21	76.5	8.5	931	2 B85062	interleukin 10 hom
22	76	8.4	179	2 A48558	hypothetical prote
23	76	8.4	1391	2 T20642	protein F09C3.1 [i
24	76	8.4	1397	2 E87998	translation elonga
25	75.5	8.4	691	2 S75863	probable hemagglut
26	75.5	8.4	3535	2 E83641	cyclin G1 interact
27	75	8.3	267	2 G02764	hypothetical prote
28	75	8.3	917	2 T05430	protein kinase hom
29	75	8.3	980	2 T05414	

30	74.5	8.3	337	2 AD3034	hypothetical prote
31	74.5	8.3	348	2 H98251	sugar ABC transpor
32	74.5	8.3	430	2 G64446	ATP-dependent 26S
33	74.5	8.3	2091	2 A97077	hypothetical prote
34	74.5	8.3	4452	1 YGBSG2	gramicidin S synth
35	74	8.2	553	2 E27793	methyl coenzyme M
36	73.5	8.1	284	2 T46694	hypothetical prote
37	73.5	8.1	361	2 A64507	hypothetical prote
38	73.5	8.1	698	2 G89787	hypothetical prote
39	73.5	8.1	1108	2 AFI271	DNA polymerase III
40	73.5	8.1	1108	2 AHI633	DNA polymerase III
41	73	8.1	309	1 S60157	RING finger protei
42	73	8.1	309	1 A57235	RING finger protei
43	73	8.1	850	2 B96839	hypothetical prote
44	73	8.1	918	2 AI0860	sensor protein [im
45	73	8.1	1071	2 F39845	carbamoyl-phosphat

ALIGNMENTS

RESULT 1

QQBE2
BCRF1 protein - human herpesvirus 4 (strain B95-8)
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999
C;Accession: A03741; S32974
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr viru
A;Reference number: A93065; MUID:85035713; PMID:6092825
A;Accession: A03741
A;Molecule type: DNA
A;Residues: 1-170 <BAN>
A;Cross-references: EMBL:V01555; NID:G59074; PIDN:CAA24863.1; PID:G59076
R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.;
Natura 310, 207-211, 1984
A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A;Reference number: A03794; MUID:84270667; PMID:6087149
A;Contents: annotation; protein coding region
C;Superfamily: interleukin-10

Query Match 11.4%; Score 103; DB 1; Length 170;
Best Local Similarity 24.8%; Pred. No. 0.024;
Matches 40; Conservative 27; Mismatches 68; Indels 26; Gaps 6;

Qy	20	CLLLALLVQGGAAAPISSHCHRLDKSNFQQ-----PYITNRTFMLAKEASLADNNTDV 72
Db	11	CLVLLYLAPECGG---TDQC-----DNFPQMLRLDLRDAFSRVKTFEFTKD-----EVDN 56
Qy	73	RLIGEKLPHGVSMSERCYLMQVNLFTLEEVLPQSDRFPQPMQEVVFFIAR-----ISNR 128
Db	57	LLKESLLEDFKGYLGCOALSEMIQPYLEEVW-PQAEHQDPEAKDHVNSLGENLKTLLR 115
Qy	129	LSTCHIEGDDLHIQRNVQKLDTVKKIGESGEIKAIGELDL 169
Db	116	LRRCHRFPCENKSKAVEQIKNAFNKIQEKGIYKAMSEFDI 156

RESULT 2

A38580
interleukin-10 precursor - human
N;Alternate names: cytokine synthesis inhibitory factor (CSIF); IL-10
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Apr-2001
C;Accession: A38580; G01539; S49110; I37890
R;Viçeira, P.; de Waal-Malefyt, R.; Dang, M.N.; Johnson, K.E.; Kastelein, R.; Fiorentin
Proc. Natl. Acad. Sci. U.S.A. 88, 1172-1176, 1991
A;Title: Isolation and expression of human cytokine synthesis inhibitory factor cDNA c
A;Reference number: A38580; MUID:91142134; PMID:1847510
A;Accession: A38580
A;Molecule type: mRNA
A;Residues: 1-178 <VIE>

Query Match 8.8%; Score 79.5; DB 2; Length 688;
Best Local Similarity 22.3%; Pred. No. 21;
Matches 42; Conservative 27; Mismatches 62; Indels 57; Gaps 8;

QY 17 ATSCLLLLALLVQGGAAAPIS--SHCRLDKSNFQQPYITNRTFMLAKEASL----- 65
Db 129 AASATLFLAHI-----APIKSVSACRI--ARVDNEFIINPSASLLNQSSLDLFFVSGTKE 180

QY 66 ADNNTDVRLLIGEKL-----FHGVSMSERCYLMKQVLFNFTLEEVLPQSDRF- 111
Db 181 SLNMIEMRSLGQKLNALAEPLMLEALELAQKSLKETCALYEEAFTPYQNELLFKEGEGIV 240

QY 112 -----QPYMQEVPVFFIARISNRLSTCHIEGDDLHIQNVQKLKDTVKKIGESGEI 161
Db 241 LNERLLDLKNQYFDEIIK-----GIESSALSRENV--FXEVAKKISEAHSE 286

QY 162 KAIGELD 169
Db 287 FSLEEIE 294

RESULT 13
E64671
polynucleotide phosphorylase - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 27-Oct-2003
C:Accession: E64671
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glödek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: E64671
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-688 <TOM>
A:Cross-references: GB:AB000627; GB:AE000511; NID:G2314373; PIDN:AAD08258.1; PID:G231437
C:Superfamily: polynucleotide nucleotidyltransferase

Query Match 8.8%; Score 79.5; DB 2; Length 688;
Best Local Similarity 21.4%; Pred. No. 21;
Matches 39; Conservative 28; Mismatches 60; Indels 55; Gaps 7;

QY 17 ATSCLLLLALLVQGGAAAPIS--SHCRLDKSNFQQPYITNRTFMLAKEASL----- 65
Db 129 AASATLFLAHI-----APIKSVSACRI--ARMDNEFIINPSASLLNQSSLDLFFVSGTKE 180

QY 66 ADNNTDVRLLIGEKL-----FHGVSMSERCYLMKQVLFNFTLEEVLPQSDRF- 111
Db 181 SLNMIEMRSLGQKLNALAEPLMLEALELAQKSLKETCTLYEIFTPHQNELFFKESQGIV 240

QY 112 -----QPYMQEVPVFFIA-----RISNRLSTCHIEGDDLHIQNVQKLK 149
Db 241 FNERLLDLKNQYFDEIIK-----GIESSALSRENVFNEIARKISEAHSEFSLEIEISLEKVK 300

QY 150 DT 151
Db 301 KT 302

RESULT 14
S50608
hypothetical protein YER105c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 23-Mar-2001
C:Accession: S50608
R:Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmid 9747, 8198, 9781, and lambda clones
A:Reference number: S50436

A:Accession: S50608
A:Molecule type: DNA
A:Residues: 1-1391 <DIE>
A:Cross-references: EMBL:U18839; NID:G603313; PIDN:AAB64660.1; PID:G603343; MIPS:YER1
C:Genetics:
A:Gene: SGD:NUP157
A:Cross-references: SGD:S0000907; MIPS:YER105c
A:Map position: 5R

Query Match 8.8%; Score 79.5; DB 2; Length 1391;
Best Local Similarity 23.7%; Pred. No. 48;
Matches 28; Conservative 25; Mismatches 48; Indels 17; Gaps 5;

QY 1 MAALQKSVSFLMGTIATSCLLLLALLVQGGAAPI---SSHCRLDKSNF---QQPYITN 54
Db 342 ISQLEVDQSRGVLHTLSTKSVRSYLTSTNGLVGPVLIDAAHRRGMNALGVKNPPLSN 401

QY 55 RTFMLAK--EASLADNN---TDVRLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLP 106
Db 402 RAFKIAKIVSISMCENNDLFLAVITTTGVRLYFKGSISRR-----SIGSLKLDVSKFP 454

RESULT 15
S59996
AMP deaminase (EC 3.5.4.6) 2 isoform L - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999
C:Accession: S59996
R:van den Bergh, F.; Sabina, R.L.
Biochem. J. 312, 401-410, 1995
A:Title: Characterization of human AMP deaminase 2 (AMPD2) gene expression reveals al
A:Reference number: S59994; MUID:96103174; PMID:8526848
A:Accession: S59996
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-605 <VAN>
A:Cross-references: EMBL:U16269; NID:G608496; PIDN:AAB06511.1; PID:G608497
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
C:Genetics:
A:Introns: 175/1; 222/2; 360/3; 404/3
C:Superfamily: AMP deaminase
C:Keywords: alternative splicing; hydrolase

Query Match 8.7%; Score 78.5; DB 2; Length 605;
Best Local Similarity 25.7%; Pred. No. 22;
Matches 38; Conservative 28; Mismatches 63; Indels 19; Gaps 8;

QY 22 LLLALLVQGGAAPISSHC--RLD--KSNFQQPYITNRTFMLAKEASLADNN-TDVRLLIG 76
Db 242 VLMALIING-----PIKSFYRRLOYLSSKFQMHVLLNEMKELAAQKKVPHRDFYNIKVD 297

QY 77 EKLFGVSMSERCYL--MKQVLFNFTLEEVLPQSDRFQPYMQEVPVFFIARISNRLSTCHI 134
Db 298 THIHASSCMNQKHLRPIKRAMKRHLEEIVHVEQGREGT-LREVFESMNLTAVDLS---V 353

QY 135 EGDDLHIQNV-----QKLDKDTVKKIGES 158
Db 354 DTLDVHADRNTHFRFDKFNKYNPIGES 381

Search completed: June 30, 2004, 19:33:29
Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 19:15:53 ; Search time 43 Seconds
(without alignments)
1176.843 Million cell updates/sec

Title: US-10-050-552A-2

Perfect score: 903

Sequence: 1 MAALQKSVSSFLMGTATSC.....EIKAGELDLFMSLRNACI 179

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1166195 seqs, 282705291 residues

Total number of hits satisfying chosen parameters: 1166195

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	903	100.0	179	13	US-10-050-552A-2
2	903	100.0	179	15	US-10-238-965-2
3	897	99.3	179	9	US-09-728-911-15
4	897	99.3	179	9	US-09-870-574-2
5	897	99.3	179	9	US-09-965-528-18
6	897	99.3	179	10	US-09-925-055D-8
7	897	99.3	179	10	US-09-746-375-2
8	897	99.3	179	12	US-10-081-056-354
9	897	99.3	179	12	US-10-219-535-244
10	897	99.3	179	12	US-10-232-230-244
11	897	99.3	179	12	US-09-969-984-18
12	897	99.3	179	12	US-10-063-745-154
13	897	99.3	179	12	US-10-063-512-154
14	897	99.3	179	12	US-10-063-513-154
15	897	99.3	179	12	US-10-063-515-154

16	897	99.3	179	12	US-10-063-549-154	Sequence 154, App
17	897	99.3	179	12	US-10-063-569-154	Sequence 154, App
18	897	99.3	179	12	US-10-063-551-154	Sequence 154, App
19	897	99.3	179	12	US-10-063-555-154	Sequence 154, App
20	897	99.3	179	12	US-10-063-563-154	Sequence 154, App
21	897	99.3	179	12	US-10-063-594-154	Sequence 154, App
22	897	99.3	179	12	US-10-063-553-154	Sequence 154, App
23	897	99.3	179	12	US-10-063-554-154	Sequence 154, App
24	897	99.3	179	12	US-10-232-224-244	Sequence 244, App
25	897	99.3	179	12	US-10-305-654-354	Sequence 354, App
26	897	99.3	179	13	US-10-006-867-154	Sequence 154, App
27	897	99.3	179	13	US-10-066-500-126	Sequence 126, App
28	897	99.3	179	13	US-10-063-547-154	Sequence 154, App
29	897	99.3	179	14	US-10-063-616-154	Sequence 154, App
30	897	99.3	179	14	US-10-063-502-154	Sequence 154, App
31	897	99.3	179	14	US-10-227-884-244	Sequence 244, App
32	897	99.3	179	14	US-10-002-796-126	Sequence 126, App
33	897	99.3	179	14	US-10-066-273-126	Sequence 126, App
34	897	99.3	179	14	US-10-066-494-126	Sequence 126, App
35	897	99.3	179	14	US-10-230-163-244	Sequence 244, App
36	897	99.3	179	14	US-10-066-269-126	Sequence 126, App
37	897	99.3	179	14	US-10-066-211-126	Sequence 126, App
38	897	99.3	179	14	US-10-066-193-126	Sequence 126, App
39	897	99.3	179	14	US-10-230-338-244	Sequence 244, App
40	897	99.3	179	14	US-10-218-631-244	Sequence 244, App
41	897	99.3	179	14	US-10-063-518-154	Sequence 154, App
42	897	99.3	179	14	US-10-230-414-244	Sequence 244, App
43	897	99.3	179	14	US-10-063-598-154	Sequence 154, App
44	897	99.3	179	14	US-10-227-693-154	Sequence 154, App
45	897	99.3	179	14	US-10-063-567-154	Sequence 154, App

ALIGNMENTS

RESULT 1
US-10-050-552A-2
; Sequence 2, Application US/10050552A
; Publication No. US20020187512A1
; GENERAL INFORMATION:
; APPLICANT: Nagem, Ronaldo A.P.
; APPLICANT: Colau, Didier
; APPLICANT: Renauld, Jean-Christophe
; APPLICANT: Dumoutier, Laure
; APPLICANT: Polikarpov, Igor
; TITLE OF INVENTION: Crystal Structure of Interleukin-22
; FILE REFERENCE: LUD-5722 US
; CURRENT APPLICATION NUMBER: US/10/050,552A
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/317,937
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/333,150
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 179
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-050-552A-2

Query Match 100.0%; Score 903; DB 13; Length 179;
Best Local Similarity 100.0%; Pred. No. 9e-92;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSSFLMGTATSCLLLLALVQGGAAAPISSHCRLDKSNFQFPYITNRTFMLA 60

Db 1 MAALQKSVSSFLMGTATSCLLLLALVQGGAAAPISSHCRLDKSNFQFPYITNRTFMLA 60

QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPMQEVVP 120

Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPMQEVVP 120

QY 121 FIARISNRLSTCHIEGDDHLIQRNVQKLKDTVKKIGESGEIKAI GELDLFLFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDHLIQRNVQKLKDTVKKIGESGEIKAI GELDLFLFMSLRNACI 179

RESULT 2

US-10-238-965-2
; Sequence 2, Application US/10238965
; Publication No. US20040002586A1
; GENERAL INFORMATION:
; APPLICANT: Nagem, Ronaldo A.P.
; APPLICANT: Colau, Didier
; APPLICANT: Renauld, Jean-Christophe
; APPLICANT: Dumoutier, Laure
; APPLICANT: Polikarpov, Igor
; TITLE OF INVENTION: Crystal Structure of Interleukin-22
; FILE REFERENCE: LUD-5722 US
; CURRENT APPLICATION NUMBER: US/10/238,965
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/317,937
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/333,150
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 179
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-238-965-2

Query Match 100.0%; Score 903; DB 15; Length 179;
Best Local Similarity 100.0%; Pred. No. 9e-92;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSSFLMGTATSCLLLLALLVQGGAAAPISSHCHRLDKSNFQOPYITNRTFMLA 60
Db 1 MAALQKSVSSFLMGTATSCLLLLALLVQGGAAAPISSHCHRLDKSNFQOPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDHLIQRNVQKLKDTVKKIGESGEIKAI GELDLFLFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDHLIQRNVQKLKDTVKKIGESGEIKAI GELDLFLFMSLRNACI 179

RESULT 3

US-09-728-911-15
; Sequence 15, Application US/09728911
; Patent No. US20020012669A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 99-93
; CURRENT APPLICATION NUMBER: US/09/728,911
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/169,049
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 60/232,219
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/244,610
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 903; DB 15; Length 179;
Best Local Similarity 100.0%; Pred. No. 9e-92;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDHLIQRNVQKLKDTVKKIGESGEIKAI GELDLFLFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDHLIQRNVQKLKDTVKKIGESGEIKAI GELDLFLFMSLRNACI 179

US-09-728-911-15

Query Match 99.3%; Score 897; DB 9; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSSFLMGTATSCLLLLALLVQGGAAAPISSHCHRLDKSNFQOPYITNRTFMLA 60
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Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
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Db 121 FIARISNRLSTCHIEGDDHLIQRNVQKLKDTVKKIGESGEIKAI GELDLFLFMSLRNACI 179

RESULT 4

US-09-870-574-2
; Sequence 2, Application US/09870574
; Patent No. US20020102723A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Austin L.
; APPLICANT: Aggarwal, Sudeepa
; APPLICANT: Xie, Ming-Hong
; APPLICANT: Maruoka, Ellen M.
; APPLICANT: Foster, Jessica S.
; APPLICANT: Goddard, Audrey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: INTERLEUKIN-22 POLYPEPTIDES, NUCLEIC ACIDS ENCODING
; FILE REFERENCE: P2806-1(US)
; CURRENT APPLICATION NUMBER: US/09/870,574
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 60/169,495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 2
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-870-574-2

Query Match 99.3%; Score 897; DB 9; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSSFLMGTATSCLLLLALLVQGGAAAPISSHCHRLDKSNFQOPYITNRTFMLA 60
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QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDHLIQRNVQKLKDTVKKIGESGEIKAI GELDLFLFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDHLIQRNVQKLKDTVKKIGESGEIKAI GELDLFLFMSLRNACI 179

RESULT 5

US-09-965-528-18
; Sequence 18, Application US/09965528
; Publication No. US20020187523A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. Tom

Query Match 99.3%; Score 897; DB 9; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSSFLMGTATSCLLLLALLVQGGAAAPISSHCHRLDKSNFQOPYITNRTFMLA 60
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Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
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Db 121 FIARISNRLSTCHIEGDDHLIQRNVQKLKDTVKKIGESGEIKAI GELDLFLFMSLRNACI 179

APPLICANT: YUE, Henry
APPLICANT: LAL, Preeti
APPLICANT: BURFORD, Neil
APPLICANT: BANDMAN, Olga
APPLICANT: BAUGHN, Mariah R.
APPLICANT: AZIMZAI, Yalda
APPLICANT: LU, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
FILE REFERENCE: PE-0701 USA
CURRENT APPLICATION NUMBER: US/09/965,528
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/134,949
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/144,270
PRIOR FILING DATE: 1999-07-15
PRIOR APPLICATION NUMBER: 60/146,700
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/157,508
PRIOR FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PERL Program
SEQ ID NO 18
LENGTH: 179
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020187523A1 5571181CD1
US-09-965-528-18

Query Match 99.3%; Score 897; DB 9; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAAPISSHCHRLDKSNFQOPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEEVLPQSDRFQPYMQEVVP 120
DB 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEEVLPQSDRFQPYMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDHLHIQNVQKLDKTVKKIGESGEIKAIGELDLLEFMSLRNACI 179
DB 121 FLARLSNRLSTCHIEGDDHLHIQNVQKLDKTVKKIGESGEIKAIGELDLLEFMSLRNACI 179

RESULT 6

US-09-925-055D-8
Sequence 8, Application US/09925055D
Publication No. US20030157096A1
GENERAL INFORMATION:
APPLICANT: Kindsvogel, Wayne R.
APPLICANT: Topouzis, Stavros
TITLE OF INVENTION: SOLUBLE ZCYTOR11 CYTOKINE RECEPTORS
FILE REFERENCE: 00-56
CURRENT APPLICATION NUMBER: US/09/925,055D
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/223,827
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: US 60/250,876
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 179
TYPE: PRT
ORGANISM: homo sapiens
US-09-925-055D-8

Query Match 99.3%; Score 897; DB 10; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;

Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAAPISSHCHRLDKSNFQOPYITNRTFMLA 60
DB 1 MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAAPISSHCHRLDKSNFQOPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEEVLPQSDRFQPYMQEVVP 120
DB 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEEVLPQSDRFQPYMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDHLHIQNVQKLDKTVKKIGESGEIKAIGELDLLEFMSLRNACI 179
DB 121 FLARLSNRLSTCHIEGDDHLHIQNVQKLDKTVKKIGESGEIKAIGELDLLEFMSLRNACI 179

RESULT 7

US-09-746-375-2
Sequence 2, Application US/09746375
Publication No. US20030170823A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Kindsvogel, Wayne
TITLE OF INVENTION: NOVEL CYTOKINE ZCYTO18
FILE REFERENCE: 99-106
CURRENT APPLICATION NUMBER: US/09/746,375
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 60/172,105
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/****,***
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 179
TYPE: PRT
ORGANISM: Homo sapiens
US-09-746-375-2

Query Match 99.3%; Score 897; DB 10; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAAPISSHCHRLDKSNFQOPYITNRTFMLA 60
DB 1 MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAAPISSHCHRLDKSNFQOPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEEVLPQSDRFQPYMQEVVP 120
DB 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVNLFTLEEVLPQSDRFQPYMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDHLHIQNVQKLDKTVKKIGESGEIKAIGELDLLEFMSLRNACI 179
DB 121 FLARLSNRLSTCHIEGDDHLHIQNVQKLDKTVKKIGESGEIKAIGELDLLEFMSLRNACI 179

RESULT 8

US-10-081-056-354
Sequence 354, Application US/10081056
Publication No. US20040043927A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.
APPLICANT: Williams, P. Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235P1C1
CURRENT APPLICATION NUMBER: US/10/081,056
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/230,978
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/000,000
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 09/664,610
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/242,922
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 09/709,238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30952
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/747,259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/767,609
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/796,498
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: US 09/802,706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/808,689
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 09/816,744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 09/828,366
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 09/854,208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/854,280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/866,034
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/US01/17092

PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/870,574
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17443
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/00000
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 354
LENGTH: 179
TYPE: PRT
ORGANISM: Homosapiens
US-10-081-056-354
Query Match 99.3%; Score 897; DB 12; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAALQKSVSSFLMGTLSCLLLALLVQGGAAAPISSHCHRLDKSNFQOPYITNRTFMLA 60
Db 1 MAALQKSVSSFLMGTLSCLLLALLVQGGAAAPISSHCHRLDKSNFQOPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVNLFTLEEVLPQSDRFQPYMQEVVP 120
Db 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVNLFTLEEVLPQSDRFQPYMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDLHIQNVQKLKDTVKKIGSGEIKAI GELDLLFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDLHIQNVQKLKDTVKKIGSGEIKAI GELDLLFMSLRNACI 179
RESULT 9
US-10-219-535-244
Sequence 244, Application US/10219535
Publication No. US20040044179A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C60
CURRENT APPLICATION NUMBER: US/10/219,535
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656


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; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 179
; SEQ ID NO 154
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-745-154

Query Match 99.3%; Score 897; DB 12; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAPISSHCRDKSNFQQPYITNRTFMLA 60
Db 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAPISSHCRDKSNFQQPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
Db 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
QY 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAIGELDLFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAIGELDLFMSLRNACI 179

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 179
; SEQ ID NO 154
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-745-154

Query Match 99.3%; Score 897; DB 12; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAPISSHCRDKSNFQQPYITNRTFMLA 60
Db 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAPISSHCRDKSNFQQPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
Db 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
QY 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAIGELDLFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAIGELDLFMSLRNACI 179

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 179
; SEQ ID NO 154
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-512-154

Query Match 99.3%; Score 897; DB 12; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAPISSHCRDKSNFQQPYITNRTFMLA 60
Db 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAPISSHCRDKSNFQQPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
Db 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
QY 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAIGELDLFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAIGELDLFMSLRNACI 179

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 179
; SEQ ID NO 154
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-512-154

Query Match 99.3%; Score 897; DB 12; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAPISSHCRDKSNFQQPYITNRTFMLA 60

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Db 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAPISSHCRDKSNFQQPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
Db 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
QY 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAIGELDLFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAIGELDLFMSLRNACI 179

RESULT 14
US-10-063-513-154
; Sequence 154, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 179
; SEQ ID NO 154
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-513-154

Query Match 99.3%; Score 897; DB 12; Length 179;
Best Local Similarity 98.3%; Pred. No. 4.2e-91;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAPISSHCRDKSNFQQPYITNRTFMLA 60
Db 1 MAALQKSVSSFLMGTLATSCILLALLVQGGAAPISSHCRDKSNFQQPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
Db 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVP 120
QY 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAIGELDLFMSLRNACI 179
Db 121 FIARISNRLSTCHIEGDDLHIQNVQKLDKTVKKIGESGEIKAIGELDLFMSLRNACI 179

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1

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US-10-063-515-154
; Sequence 154, Application US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1

RESULT 15
US-10-063-515-154
; Sequence 154, Application US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1

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Search completed: June 30, 2004, 19:29:39
Job time : 44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 19:14:58 ; Search time 59 Seconds
(without alignments)
857.220 Million cell updates/sec

Title: US-10-050-552A-2
Perfect score: 903
Sequence: 1 MAALQKSVSSFLMGTLATSC.....EIKAGELDLLEMSLENAEI 179

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	897	99.3	179	3	AAY92879 Human T C
2	897	99.3	179	3	AAB36292 Human GIL
3	897	99.3	179	4	AAB31210 Amino aci
4	897	99.3	179	4	AAB04538 Human cyt
5	897	99.3	179	4	AAB87602 Human PRO
6	897	99.3	179	4	AAB62664 Human IL-
7	897	99.3	179	4	AAB48074 Human ext
8	897	99.3	179	5	AAB3713 Human PRO
9	897	99.3	179	5	AAB19237 Human TIF
10	897	99.3	179	5	ABG95927 Human sec
11	897	99.3	179	5	ABB84993 Human PRO
12	897	99.3	179	5	AAU78081 Human int
13	897	99.3	179	5	AAE28608 Human IL-
14	897	99.3	179	5	AAU76909 Human int
15	897	99.3	179	5	ABB95599 Human ang
16	897	99.3	179	5	ABB79910 Human int
17	897	99.3	179	6	ABU80860 Human PRO
18	897	99.3	179	6	ABO25181 Novel hum
19	897	99.3	179	6	ABO33826 Novel hum
20	897	99.3	179	6	ABU90952 Novel hum
21	897	99.3	179	6	ABO34011 Human sec
22	897	99.3	179	6	ABU72028 Novel hum
23	897	99.3	179	6	ABU67299 Novel hum
24	897	99.3	179	6	ABU71582 Human sec
25	897	99.3	179	6	ABU72363 Human PRO

26	897	99.3	179	6	ABU91036 Human PRO
27	897	99.3	179	6	ABO27357 Human sec
28	897	99.3	179	6	ABU72067 Novel hum
29	897	99.3	179	6	ABU67168 Novel hum
30	897	99.3	179	6	ABU92552 Human sec
31	897	99.3	179	6	ABU81222 Human sec
32	897	99.3	179	6	ABU82169 Novel hum
33	897	99.3	179	6	ABO53336 Novel hum
34	897	99.3	179	6	AAE30833 Human int
35	897	99.3	179	6	ABU98339 Novel hum
36	897	99.3	179	6	ABU89344 Novel hum
37	897	99.3	179	6	ABU82551 Novel hum
38	897	99.3	179	6	ABU96515 Human PRO
39	897	99.3	179	6	ABU72185 Human PRO
40	897	99.3	179	6	ABU79810 Human sec
41	897	99.3	179	6	ABJ72349 Human PRO
42	897	99.3	179	6	ADB17211 Human tra
43	897	99.3	179	6	ABO44315 Human sec
44	897	99.3	179	6	ADA20016 Novel hum
45	897	99.3	179	6	ADB17399 Human tra

ALIGNMENTS

RESULT 1
AAY92879
ID AAY92879 standard; protein; 179 AA.
XX
AC AAY92879;
XX
DT 04-SEP-2000 (first entry)
XX
DE Human T cell inducible factor.
XX
KW TIF; T cell derived inducible factor; interleukin 9; STAT; IL-9;
KW Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist;
KW Chromosome 12q15.
XX
OS Homo sapiens.
XX
PN WO200024758-A1.
XX
PD 04-MAY-2000.
XX
PF 18-OCT-1999; 99WO-US024424.
XX
PR 26-OCT-1998; 98US-00178973.
PR 16-JUL-1999; 99US-00354243.
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Dumoutier L, Louhed J, Renauld J;
XX
DR WPI; 2000-422495/36.
DR N-PSDB; AAA28839, AAA28840.
XX
PT New nucleic acid molecule encoding a T cell derived inducible factor for
XX treating asthma, an allergy or lymphoma.
PS Example 26; Fig 1; 46pp; English.
XX
CC This is the human T cell derived inducible factor (TIF). The gene was
CC mapped to chromosome 12q15. The human TIF was identified based on
CC homology to a murine TIF, which was identified by subtraction cloning
CC from a murine lymphoma cell line BW5147 in the presence or absence of
CC interleukin 9 (IL-9). BW5147, can be grown in vitro, without the need to
CC add any cytokines to its culture medium. Many IL-9 activities are
CC mediated by activation of STAT transcription factors. The novel TIFs were
CC expressed in the presence of IL-9, but not in its absence. TIFs induce
CC STAT activation in cells. They can be used, e.g. in the stimulation of
CC regeneration of targeted tissues. Their inhibitors or antagonists can be
CC used to retard, prevent or inhibit differentiation of other tissues. The

PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
XX
PA (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL,
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AJ, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams EM;
PI Wood WI, Zhang Z;
XX
XX WPI; 2001-050091/06.
DR N-PSDB; AAC87053.
XX
PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT transmembrane polypeptide is useful for gene therapy and identification
PT of related polypeptides.
XX
XX Claim 12; Fig 64; 244pp; English.
PS
CC The present sequence represents a human secreted and transmembrane
CC polypeptide. The specification describes human polypeptides, designated
CC PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
CC PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO1096, PRO6003,
CC PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC can be modulated with agents that bind to these polypeptides, resulting
CC in the death of the cells. The polynucleotides encoding these
CC polypeptides are useful in the recombinant production of the
CC polypeptides, as a hybridisation probe to screen libraries to isolate
CC homologous sequences, or to map the gene. They may also be used for
CC analysing genetic disorders, and to produce transgenic animals which are
CC useful for the development and screening of therapeutically useful
CC reagents. The polynucleotides can also be used in gene therapy e.g. to
CC replace a defective gene
XX
SQ Sequence 179 AA;

Query Match 99.3%; Score 897; DB 4; Length 179;
Best Local Similarity 98.3%; Pred. No. 8.7e-87;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAPISSHCHRLDKSNFQOPYITNRTFMLA 60
Db 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAPISSHCHRLDKSNFQOPYITNRTFMLA 60
Qy 61 KEASLADNNTDVRLLIGKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
Db 61 KEASLADNNTDVRLLIGKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
Qy 121 FLARISNRLSTCHIEGDDHLHIQRNVQKLKDTVKKIGESGEIKAIGELDLFLFMSLRNACI 179
Db 121 FLARISNRLSTCHIEGDDHLHIQRNVQKLKDTVKKIGESGEIKAIGELDLFLFMSLRNACI 179

RESULT 4
AAE04538
ID AAE04538 standard; protein; 179 AA.
XX
AC AAE04538;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human cytokine, ZCYTO18 protein #1.
XX
KW Human; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;
KW cancer; inflammation; gene therapy.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT Peptide 1..33
FT /label= Signal_peptide
FT Protein 34..179
FT /label= Mature_ZCYTO18_protein
FT Region 145..150
FT /label= Hydrophilic_region
XX
XX WO200146422-A1.
PN
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000WO-US035308.
XX
PR 23-DEC-1999; 99US-00471767.
PR 01-DEC-2000; 2000US-0250841P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Kindsvogel W;
XX
DR WPI; 2001-408648/43.
XX N-PSDB; AAD09719.
PT Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer.
XX
PS Claim 4; Page 142; 167pp; English.
XX
CC The patent discloses novel human cytokine, ZCYTO18 protein and its
CC corresponding DNA. ZCYTO18 protein induces proliferation of cells
CC expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity in
CC K5626 cells. ZCYTO18 DNA is useful for detecting a genetic abnormality in
CC a patient. ZCYTO18 DNA and its antibodies are useful for detecting cancer
CC and inflammation. ZCYTO18 protein is useful for killing cancer cells. It
CC is useful for increasing platelets in a patient or injured tissue. It is
CC also used in gene therapy. The present sequence is novel human cytokine,
CC ZCYTO18 protein
XX
SQ Sequence 179 AA;

Query Match 99.3%; Score 897; DB 4; Length 179;
Best Local Similarity 98.3%; Pred. No. 8.7e-87;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAPISSHCHRLDKSNFQOPYITNRTFMLA 60
Db 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAPISSHCHRLDKSNFQOPYITNRTFMLA 60
Qy 61 KEASLADNNTDVRLLIGKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
Db 61 KEASLADNNTDVRLLIGKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
Qy 121 FLARISNRLSTCHIEGDDHLHIQRNVQKLKDTVKKIGESGEIKAIGELDLFLFMSLRNACI 179
Db 121 FLARISNRLSTCHIEGDDHLHIQRNVQKLKDTVKKIGESGEIKAIGELDLFLFMSLRNACI 179

RESULT 5
AAB87602
ID AAB87602 standard; protein; 179 AA.
XX
AC AAB87602;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO10096.
XX
KW Human; PRO protein; mapping.
XX
OS Homo sapiens.
XX
PN WO200116318-A2.
XX

PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US023328.
XX
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 07-DEC-1999; 99US-0169495P.
PR 09-DEC-1999; 99US-0170262P.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 03-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000WO-US008439.
PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX

(GETH) GENENTECH INC.

PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AJ, Watanabe CK, Wood WI;
XX

DR WPI; 2001-183260/18.
DR N-PSDB; AAF92134.

XX
PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
XX gene mapping.

PS Claim 12; Fig 154; 278pp; English.

XX
CC The present sequence is a human PRO polypeptide (secreted and
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC anti-PRO antibodies are useful for preparation of a medicament useful in
CC the treatment of a condition which is responsive to the PRO protein,
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC employed as molecular weight markers for protein electrophoresis. The PRO
CC coding sequence has applications in molecular biology, including use as
CC hybridisation probes, and in chromosome and gene mapping
XX

SQ Sequence 179 AA;

Query Match 99.3%; Score 897; DB 4; Length 179;
Best Local Similarity 98.3%; Pred. No. 8.7e-87;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSFLMGTATSCLLALLVQGGAAPISSHCRDLSNFFQPYITNRTFMLA 60
Db
1 MAALQKSVSFLMGTATSCLLALLVQGGAAPISSHCRDLSNFFQPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDHLHQRNVQKLKDTVKKIGESGEIKAGELDLFLMSLRNACI 179
Db 121 FLARLSNRLSTCHIEGDDHLHQRNVQKLKDTVKKIGESGEIKAGELDLFLMSLRNACI 179

RESULT 6

AAB62664
ID AAB62664 standard; protein; 179 AA.

XX AAB62664;

XX 23-JUL-2001 (first entry)

XX Human IL-TIF polypeptide.

DE Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic;
KW

KW antirheumatic; antiarthritic; antiasthmatic; antiatherosclerotic;
XX immunosuppressive; chromosome 6q24.1-25.2; human.

OS Homo sapiens.

XX WO200140467-A1.

PN 07-JUN-2001.

XX 01-DEC-2000; 2000WO-US032703.

XX 03-DEC-1999; 99US-0169049P.

PR 13-SEP-2000; 2000US-0232219P.

PR 31-OCT-2000; 2000US-0244610P.

XX (ZYMO) ZYMOGENETICS INC.

XX Presnell SR, Xu W, Kindsvogel W, Chen Z;

XX WPI; 2001-356158/37.

DR N-PSDB; AAF83741.

XX New soluble cytokine receptor polypeptides and polynucleotides, useful
PT for diagnosing and treating cancer and inflammatory conditions.

XX Example 17; Page 195-196; 210pp; English.

CC The invention relates to a human cytokine receptor polypeptide,
CC designated zcytor16. The zcytor16 polypeptide can be expressed by
CC standard recombinant methodology and can bind to IL-TIF (undefined). The
CC zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation
CC or differentiation of hematopoietic cell(s) (progenitors); reducing IL-
CC TIF induced or IL-9 induced inflammation; and suppressing an inflammatory
CC response in a mammal with inflammation. Heteromeric/ multimeric receptor
CC polypeptides such as soluble zcytor 16/CRP2-4 can be used to reduce
CC progression and symptoms of cancer. Zcytor16 polypeptides can also be
CC used to detect IL-TIF levels which is indicative of pathological
CC conditions including inflammatory states (e.g. rheumatoid arthritis) and
CC cancer. Antibodies that bind zcytor16 polypeptides and the polypeptides
CC themselves are useful for the treatment of inflammation, inflammatory
CC diseases (e.g. infection, asthma, inflammatory bowel disease, rheumatoid
CC arthritis and atherosclerosis) and autoimmune diseases. The antibodies
CC and zcytor16 polynucleotides are also useful for detecting cancer. The
CC present sequence represents the human IL-TIF protein
XX

SQ Sequence 179 AA;

Query Match 99.3%; Score 897; DB 4; Length 179;
Best Local Similarity 98.3%; Pred. No. 8.7e-87;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSFLMGTATSCLLALLVQGGAAPISSHCRDLSNFFQPYITNRTFMLA 60
Db 1 MAALQKSVSFLMGTATSCLLALLVQGGAAPISSHCRDLSNFFQPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDHLHQRNVQKLKDTVKKIGESGEIKAGELDLFLMSLRNACI 179
Db 121 FLARLSNRLSTCHIEGDDHLHQRNVQKLKDTVKKIGESGEIKAGELDLFLMSLRNACI 179

RESULT 7

AAB48074
ID AAB48074 standard; protein; 179 AA.

XX AAB48074;

XX 19-MAR-2001 (first entry)

DE Human extracellular signaling molecule (EXCS) (ID 5571181CD1).

PS Claim 11; Fig 244; 359pp; English.

XX The invention relates to one hundred and twenty two nucleic acids

CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides

CC encode human secreted proteins. The PRO nucleic acids, polypeptides,

CC agonists and antagonists are useful for treating a PRO related disorder.

CC The PRO polypeptides are useful for diagnosing tumours, especially lung

CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or

CC liver tumour. The PRO polypeptides are useful for stimulating the

CC proliferation of, or gene expression, in pericyte cells, for stimulating

CC the proliferation or differentiation of chondrocyte cells, for

CC stimulating the release of tumour necrosis factor-alpha from human blood,

CC for stimulating or inhibiting the proliferation of normal human dermal

CC fibroblast cells. The PRO polypeptide may also be used as molecular

CC weight markers and for tissue typing. The PRO nucleic acids have

CC applications in molecular biology, including use as hybridisation probes,

CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO

CC protein sequences of the invention

XX

SQ Sequence 179 AA;

Query Match 99.3%; Score 897; DB 5; Length 179;

Best Local Similarity 98.3%; Pred. No. 8.7e-87;

Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQPYITNRTFMLA 60

Db 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQPYITNRTFMLA 60

QY 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120

Db 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120

QY 121 FIARISNRLSTCHIEGDDDLHIQNVQKLDTVKKIGESGEIKAIGELDLFMSLRNACI 179

Db 121 FLARLSNRLSTCHIEGDDDLHIQNVQKLDTVKKIGESGEIKAIGELDLFMSLRNACI 179

RESULT 9

AAE19237

ID AAE19237 standard; protein; 179 AA.

XX

AC AAE19237;

XX

DT 21-MAY-2002 (first entry)

XX

DE Human TIF protein.

XX

KW T cell derived inducible factor; TIF; interleukin-21; IL-21; human;

KW STAT transcription factor; acute phase protein; inflammation;

KW Chromosome 12.

XX

OS Homo sapiens.

XX

PN WO200210393-A2.

XX

PD 07-FEB-2002.

XX

PF 27-JUN-2001; 2001WO-US020485.

XX

XX 27-JUL-2000; 2000US-00626617.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

XX Dumoutier L, Renauld J;

PI

XX WPI; 2002-195964/25.

DR N-PSDB; AAD30645.

XX

XX Stimulating expression of STAT transcription factor and inducing

PT production of acute phase protein in a cell, involves contacting a cell

PT capable of expressing STAT with T cell derived inducible factors.

XX

PS Disclosure; Page 64; 64pp; English.

XX The invention relates to nucleic acid molecules encoding T cell derived

CC inducible factors (TIFs) also known as interleukin-21 (IL-21). TIF

CC polynucleotides are upregulated by the cytokine, IL-9, IL-TIF or IL-21

CC molecules are implicated in activation of STAT transcription factors,

CC acute phase proteins and inflammation. The present sequence is human TIF

CC protein. The TIF gene is located on chromosome 12

XX

SQ Sequence 179 AA;

Query Match 99.3%; Score 897; DB 5; Length 179;

Best Local Similarity 98.3%; Pred. No. 8.7e-87;

Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQPYITNRTFMLA 60

Db 1 MAALQKSVSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQPYITNRTFMLA 60

QY 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120

Db 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120

QY 121 FIARISNRLSTCHIEGDDDLHIQNVQKLDTVKKIGESGEIKAIGELDLFMSLRNACI 179

Db 121 FLARLSNRLSTCHIEGDDDLHIQNVQKLDTVKKIGESGEIKAIGELDLFMSLRNACI 179

RESULT 10

ABG95927

ID ABG95927 standard; protein; 179 AA.

XX

AC ABG95927;

XX

DT 10-DEC-2002 (first entry)

XX

DE Human secreted/transmembrane protein PRO10096.

XX

KW Human; secreted protein; transmembrane protein; antirheumatic;

KW antiarthritic; osteopathic; sports-related joint problem;

KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.

XX

OS Homo sapiens.

XX

PN US2002119130-A1.

XX

PD 29-AUG-2002.

XX

PF 06-DEC-2001; 2001US-00006867.

XX

PR 29-OCT-1997; 97US-0063435P.

PR 29-OCT-1997; 97US-0064215P.

PR 22-APR-1998; 98US-0082797P.

PR 29-APR-1998; 98US-0083495P.

PR 15-MAY-1998; 98US-0085579P.

PR 02-JUN-1998; 98US-0087759P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088029P.

PR 10-JUN-1998; 98US-0088734P.

PR 10-JUN-1998; 98US-0088740P.

PR 10-JUN-1998; 98US-0088811P.

PR 10-JUN-1998; 98US-0088824P.

PR 11-JUN-1998; 98US-0088863P.

PR 12-JUN-1998; 98US-0089105P.

PR 16-JUN-1998; 98US-0089514P.

PR 17-JUN-1998; 98US-0089653P.

PR 19-JUN-1998; 98US-0089952P.

PR 22-JUN-1998; 98US-0090246P.

PR 24-JUN-1998; 98US-0090444P.

PR 25-JUN-1998; 98US-0090688P.

PR 25-JUN-1998; 98US-0090696P.

26-JUN-1998; 98US-0090862P.
 02-JUL-1998; 98US-0091628P.
 10-AUG-1998; 98US-0096012P.
 17-AUG-1998; 98US-0096757P.
 18-AUG-1998; 98US-0096949P.
 18-AUG-1998; 98US-0096959P.
 26-AUG-1998; 98US-0097954P.
 26-AUG-1998; 98US-0097971P.
 26-AUG-1998; 98US-0097979P.
 01-SEP-1998; 98US-0098749P.
 10-SEP-1998; 98US-0099741P.
 10-SEP-1998; 98US-0099763P.
 10-SEP-1998; 98US-0099792P.
 10-SEP-1998; 98US-0099812P.
 10-SEP-1998; 98US-0099815P.
 16-SEP-1998; 98US-0100627P.
 16-SEP-1998; 98US-0100662P.
 16-SEP-1998; 98US-0100683P.
 17-SEP-1998; 98US-0100684P.
 17-SEP-1998; 98US-0100930P.
 22-SEP-1998; 98US-0101279P.
 23-SEP-1998; 98US-0101475P.
 24-SEP-1998; 98US-0101738P.
 24-SEP-1998; 98US-0101743P.
 24-SEP-1998; 98US-0101916P.
 30-SEP-1998; 98US-0102570P.
 06-OCT-1998; 98US-0103449P.
 08-MAR-1999; 99WO-US005028.
 14-MAY-1999; 99WO-US010733.
 02-JUN-1999; 99WO-US012252.
 01-SEP-1999; 99WO-US020111.
 15-SEP-1999; 99WO-US021090.
 15-SEP-1999; 99WO-US021194.
 22-DEC-1999; 99WO-US030720.
 18-FEB-2000; 2000WO-US004341.
 18-FEB-2000; 2000WO-US004342.
 22-FEB-2000; 2000WO-US004414.
 01-MAR-2000; 2000WO-US005601.
 30-MAR-2000; 2000WO-US008439.
 22-MAY-2000; 2000WO-US014042.
 02-JUN-2000; 2000WO-US015264.
 23-AUG-2000; 2000WO-US023522.
 24-AUG-2000; 2000WO-US023328.
 10-NOV-2000; 2000WO-US030873.
 01-DEC-2000; 2000WO-US032378.
 20-DEC-2000; 2000WO-US034956.
 28-FEB-2001; 2001WO-US006520.
 01-MAR-2001; 2001WO-US006666.
 30-MAY-2001; 2001WO-US017443.
 01-JUN-2001; 2001WO-US017800.
 20-JUN-2001; 2001WO-US019692.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CC, Gurney AL, Watanabe CK, Wood WL;

WPI; 2002-731348/79.
 N-PSDB; ABS74454.

New isolated secreted and transmembrane PRO polypeptide useful for modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arthritis.

Claim 20; Fig 154; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO polypeptide having 80 % sequence identity to a sequence appearing as ABG95851-ABG95934 or their associated signal peptide, or a sequence of an extracellular domain of the proteins with their associated signal peptide

or lacking its associated signal peptide. Also included are the nucleic acids encoding the proteins, vectors, host cells, fusion proteins and antibodies which specifically bind to the proteins. The proteins are useful for detecting a polypeptide designated as A, B, C or D in a sample suspected of containing an A, B, C or D polypeptide, by contacting the sample with a polypeptide designated as E, F, G, H or I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide conjugate in the sample, where the formation of the conjugate is indicative of the presence of an A, B, C or D polypeptide in the sample, where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with a detectable label or is attached to a solid support. The proteins are useful for linking a bioactive molecule to a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies against them are useful for modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I. The cell is killed. The proteins are useful for identifying agonists or antagonists, for the preparation of a medicament useful in the treatment of a condition which is responsive to the proteins, as molecular weight markers for protein electrophoresis purposes, and as therapeutic agents for treating sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. Nucleic acids encoding the proteins are useful as hybridisation probes, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, for the preparation of the proteins, to generate transgenic or knockout animals which are useful in the development and screening of therapeutic useful reagents, for chromosome identification, and in gene therapy. The antibody is useful as a therapeutic agent, in a diagnostic assay and for affinity purification of the protein from recombinant cell culture natural sources. The present sequence represents a novel secreted or transmembrane protein of the invention

XX
 SQ Sequence 179 AA;

Query Match 99.3%; Score 897; DB 5; Length 179;
 Best Local Similarity 98.3%; Pred. No. 8.7e-87;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAALQKSVSFLMGTLATSCLLALLVQGGAAAPISSHCRDKSNFQPPYITNRTFMLA 60
 |||||
 Db 1 MAALQKSVSFLMGTLATSCLLALLVQGGAAAPISSHCRDKSNFQPPYITNRTFMLA 60
 Qy 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
 |||||
 Db 61 KEASLADNNTDVRLLIGEKLFHGVSMSERCYLMKQVLFNFTLEEVLPQSDRFQPYMQEVVP 120
 Qy 121 FIARISNRLSTCHIEGDDHLHQRNVQKLKDTVKKIGESGRKAIGELDLFMSLRNACI 179
 |||||
 Db 121 FIARISNRLSTCHIEGDDHLHQRNVQKLKDTVKKIGESGRKAIGELDLFMSLRNACI 179

RESULT 11
 ABB84993

ID ABB84993 standard; protein; 179 AA.

XX
 AC ABB84993;

XX 16-MAY-2002 (first entry)

XX Human PRO10096 protein sequence SEQ ID NO:354.

XX Human; angiogenesis; cardiac; cytostatic; antiangiogenic; hypotensive;
 KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;

KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
PN W0200200690-A2.
PN
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001WO-US019692.
XX
PR 23-JUN-2000; 2000US-0213637P.
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-090516/12.
DR N-PSDB; ABL88243.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 354; 565pp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,

CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX
SQ Sequence 179 AA;
Query Match: 99.3%; Score 897; DB 5; Length 179;
Best Local Similarity 98.3%; Pred. NO. 8.7e-87;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAALQKSVSSFLMGTATSCLLLLALLVQGGAAAPISSHCRLDKSNFQPYITNRTFMLA 60
DB 1 MAALQKSVSSFLMGTATSCLLLLALLVQGGAAAPISSHCRLDKSNFQPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFHGVSMSEKCYLMKQVLFNFTLEEVLPQSDRFQPMQEVVP 120
DB 61 KEASLADNNTDVRLLIGEKLFHGVSMSEKCYLMKQVLFNFTLEEVLPQSDRFQPMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDHLIQRNVQKLDTVKKIGESGEIKAIGELDLLEFMSLRNACI 179
DB 121 FLARLSNRLSTCHIEGDDHLIQRNVQKLDTVKKLSEGEIKAIGELDLLEFMSLRNACI 179
RESULT 12
AAU78081
ID AAU78081 standard; protein; 179 AA.
XX
AC AAU78081;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human interleukin 22 (IL-22) protein sequence.
XX
KW Interleukin 22; IL-22; cytostatic; antiinflammatory; IL-22 antagonist;
KW immunotherapy; PAPI; pancreatitis associated protein; receptor; IL-22R;
KW IL-10Rbeta; bioactive molecule linkage; cell death; pancreatitis;
KW pancreatic disorder; pancreatic carcinoma; acinar cell carcinoma; human;
KW mixed cell population pancreatic carcinoma.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..33
FT /label= Signal_peptide
FT Modified-site 14..20
FT /note= "Asn is N-myristolated"
FT Protein 34..179
FT /label= Mature_human_interleukin_22_(IL_22)
FT Modified-site 54..58
FT /note= "Asn is N-glycosylated"
FT Modified-site 68..72
FT /note= "Asn is N-glycosylated"
FT Modified-site 82..88
FT /note= "Asn is N-myristolated"
FT Modified-site 97..101
FT /note= "Asn is N-glycosylated"
XX
PN W0200216611-A2.
PN
XX 28-FEB-2002.
XX
PF 30-MAY-2001; 2001WO-US017443.
XX
PR 24-AUG-2000; 2000WO-US023328.
XX
PA (GETH) GENENTECH INC.
XX
PI Aggarwal S, Foster JS, Goddard A, Gurney AL, Maruoka EM, Wood WI;
PI Xie M;
XX
DR WPI; 2002-280940/32.
DR N-PSDB; ABK11847.
XX

PT Novel isolated interleukin 22 polypeptide useful for identifying IL-22
PT agonists and antagonists that are used for treating acute pancreatitis,
PT chronic pancreatitis, pancreatic carcinoma.

02-MAR-2001; 2001US-0273035P.
27-MAR-2001; 2001US-0279232P.
(Zymo) ZYMOGENETICS INC.
Presnell SR, Xu W, Kindsvogel W, Chen Z;
WPI; 2002-698750/75.
N-PSDE; AAD45964.
New Zcytor16 polypeptide useful for treating autoimmune or inflammatory diseases, e.g. inflammatory bowel disease, rheumatoid arthritis, asthma, atherosclerosis, cancer or diabetes, or in assessing therapeutic aspects of IL-TIF.
Disclosure; Page 197-198; 221pp; English.
The invention relates to cytokine receptor designated as mouse Zcytor16 which can bind and antagonise the IL-TIF. The Zcytor16 polypeptide is useful in modulating the immune system by binding Zcytor16 ligand, and thus, preventing the binding of the ligand with endogenous Zcytor16 receptor. It is useful for studying human inflammation or immune function, or for treating autoimmune or inflammatory diseases such as inflammatory bowel disease, rheumatoid arthritis, asthma, systemic lupus erythematosus, myasthenia gravis or allergy, atherosclerosis, cancer, diabetes, glomerulonephritis or pancreatitis, or in assessing therapeutic aspects of IL-TIF, chemical therapeutics, anti-IL-TIF antibodies, anti-Zcytor16 antibodies or Zcytor16 soluble receptors. Zcytor16 DNA and the anti-mouse Zcytor16 antibody are useful as probes in detecting gene expression and gene structure, such as in the diagnosis and/or prevention of spontaneous abortions or in monitoring placental health and function. It is also used in gene therapy. The present sequence is human IL-TIF protein
Sequence 179 AA;

61	KEASLADNN	TDVRL	IGEXKL	FHGVSM	SERCYL	MMKQV	NFTL	EEVLFP	QSDRR	FQPMQ	EVVP	120
QY	FIARIS	NRLST	CHIEG	DDLIH	IRNVOK	LKOTV	KIGES	GEIKAI	GELDIL	FMSLR	NACI	179
db	ELARLS	NRLST	CHIEG	DDLIH	IRNVOK	LKOTV	KIGES	GEIKAI	GELDIL	FMSLR	NACI	179

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OS Homo sapiens.
XX
PN WO200212345-A2.
XX
PD 14-FEB-2002.
XX
PF 08-AUG-2001; 2001WO-US024838.
XX
PR 08-AUG-2000; 2000US-0223827P.
PR 01-DEC-2000; 2000US-0250876P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Kindsvogel WR, Topouzis S;
XX
DR WPI; 2002-217182/27.
XX N-PSDB; ABK10503.
XX
PT New soluble cytokine receptor which binds interleukin-T-cell inducible
PT factor and antagonizes its activity in inflammatory and immune diseases
PT such as cancer, diabetes, asthma, sepsis, psoriasis and autoimmune
PT diseases.
XX
PS Example 1; Page 98; 117pp; English.
XX
CC This invention relates to the protein and cDNA sequences of a novel
CC soluble cytokine receptor polypeptide designated zcytorII, which binds
CC interleukin-T-cell inducible factor (IL-TIF) or antagonizes IL-TIF
CC activity. The protein of the invention is useful for reducing IL-TIF- or
CC IL-9 induced inflammation, and inhibiting IL-TIF-induced proliferation.
CC The protein is also useful for suppressing an immune response in a mammal
CC exposed to an antigen or pathogen. Soluble zcytorII receptor or
CC heterodimeric polypeptide is useful for enhancing the in vivo killing of
CC target tissues by directly stimulating a zcytorII receptor-modulated
CC apoptotic pathway. IL-TIF is involved in promoting Th1-type immune
CC responses and antagonists of IL-TIF have beneficial use against diseases
CC involving such immune responses. Soluble zcytorII heterodimers are useful
CC as antagonists in inflammatory and immune diseases or conditions such as
CC pancreatitis, type I diabetes (IDDM), pancreatic cancer, Graves disease,
CC inflammatory bowel disease (IBD), Crohn's disease, colon and intestinal
CC cancer, diverticulosis, autoimmune disease (e.g. IDDM, multiple sclerosis
CC (MS), systemic lupus erythematosus (SLE), myasthenia gravis, rheumatoid
CC arthritis and IBD), sepsis, asthma, allergy and other atopic diseases,
CC psoriasis and kidney dysfunction. Soluble zcytorII receptor or
CC heterodimeric receptor polypeptides are useful in vivo or in diagnostic
CC applications to detect IL-TIF expressing cancers in vivo or in tissue
CC samples and to prepare antibodies. ZcytorII serves as a target for MAb
CC therapy of cancer where an antagonising MAb inhibits cancer growth and
CC targets immune-mediated killing. The present sequence represents the
CC interleukin-T-cell inducible factor (IL-TIF) protein, the activity of
CC this protein is inhibited by the ZcytorII protein of the invention
XX
SQ Sequence 179 AA;
Query Match 99.3%; Score 897; DB 5; Length 179;
Best Local Similarity 98.3%; Pred. No. 8.7e-87;
Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAAPISSHCHRLDKSNFQCPYITNRTFMLA 60
Db 1 MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAAPISSHCHRLDKSNFQCPYITNRTFMLA 60
QY 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVNLFTLEVPQSDRFPQYMQEVVP 120
Db 61 KEASLADNNTDVRLLIGEKLFGVSMSERCYLMKQVNLFTLEVPQSDRFPQYMQEVVP 120
QY 121 FIARISNRLSTCHIEGDDDLHIQRNVQKLKDTVKKIGESGEIKAIGELDLFLMSLRNACI 179
Db 121 FLARLSNRLSTCHIEGDDDLHIQRNVQKLKDTVKKIGESGEIKAIGELDLFLMSLRNACI 179
RESULT 15
ABB95599
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ID ABB95599 standard; protein; 179 AA.
XX
AC ABB95599;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related protein PRO10096 SEQ ID NO: 354.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US021735.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 38-NOV-2000; 2000US-00709238.
PR 38-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 31-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 31-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX
PA (GETH ) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
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